

## FIGURE 1

CCAATGCCCGGTGCGGTGGTGCAGGGCTCGGGCTAGTC**ATG**GCCTCCCCGTCTCGGAGAC  
TGCAGACTAAACCAGTCATTACTTGTTCAGAGAGCGTTCTGCTAATCTACACTTTATTTTC  
TGGATCACTGGCGTTATCCTCTTGAGTTGGCATTGGGGCAAGGTGAGCCTGGAGAATTA  
CTTTCTCTTTAAATGAGAAGGCCACCAATGTCCCCTCGTGCTCATTGCTACTGGTACCG  
TCATTATTCTTTGGGCACCTTGGTTGTTGCTACCTGCCAGCTCTGCATGGATGCTA  
AAACTGTATGCAATGTTCTGACTCTCGTTTTGGTCGAAGTGGCGCTGCCATCGTAGG  
ATTGTTTCAGACATGAGATTAAGAACAGCTTAAGAATAATTATGAGAAGGCTTGAAGC  
AGTATAACTCTACAGGAGATTATAGAACGCATGCAGTAGACAAGATCCAAAATACGTTGCAT  
TGTGTGGTGTACCGATTATAGAGATTGGACAGATACTAATTATTACTCAGAAAAAGGATT  
TCCTAAGAGTTGCTGTAACCTGAAGATTGTACTCCACAGAGAGATGCAGACAAAGTAAACA  
ATGAAGGTTGTTTATAAAGGTGATGACCATTATAGAGTCAGAAATGGGAGTCGTTGCAGGA  
ATTTCCTTGGAGTTGCTTGCCTCAACTGATTGGAATCTTCTGCCTACTGCCWCTCTCG  
TGCCATAACAAATAACCAAGTATGAGATAGT**GTA**CCCAATGTATCTGTGGCCTATTCCCT  
CTACCTTAAGGACATTAGGGTCCCCCTGTGAATTAGAAAGTTGCTTGGCTGGAGAACTG  
ACAACACTACTGATAGACCAAAAAACTACACCAAGTAGGTTGATTCAATCAAGATGTAT  
GTAGACCTAAACTACACCAATAGGCTGATTCAATCAAGATCCGTGCTCGCAGTGGGCTGAT  
TCAATCAAGATGTATGTTGCTATGTTCTAAGTCCACCTCTATCCCATTGTTAGATCG  
TTGAAACCCGTATCCCTCTGAAACACTGGAAGAGCTAGTAAATTGTAATGAAGT

## **FIGURE 2**

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA19902
><subunit 1 of 1, 245 aa, 1 stop, 1 unknown
><MW: -1, pI: 8.36, NX(S/T): 1
MASPSRRLQTKPVITCFKSVL LIYTFIFWITGVILLAVGIWGKVSLEN YFSLLNEKATNVPF
VLIATGTVI ILLGTFGCFATCRASAWMLKLYAMFLTLVFLVELVAAIVGFVFRHEIKNSFKN
NYEKALKQYNSTGDYRSHAVDKIQNTLHCCGVTDYRDWTDTNYYSEKGFPKSCCKLEDCTPQ
RDADKVNNEGCFIKVMTII ESEMGVVAGISFGVACFQLIGIFLAYCXSRAITNNQYEIV
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-42

**Transmembrane domains:**

amino acids 19-42, 61-83, 92-114, 209-230,

**N-glycosylation site.**

amino acids 134-138

**Tyrosine kinase phosphorylation site.**

amino acids 160-168, 160-169

**N-myristoylation site.**

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 69-80, 211-222

## **FIGURE 3**

CCCACCGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTGCCGTTCTCGGACCTGTACAAA  
 GGAGTCGCGCCGCCGGCCGCCCCCTCCCTCCGGTGGGCCGGGAGGTAGAGAAAGTCAGT  
 GCCACAGCCCGACC CGC GTG CT GAG CC CT GGG CAC GCG GA AC GGG AGG GAG T CT GAG GGT  
 TGGGGACGTCTGTGAGGGAGGGAACAGCCGCTCGAGCCTGGGC GGG CGG ACC GG ACT GGG  
 GCCGGGGTAGGCTCTGAAAGGGCCGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA  
 GCCGAGAGGTTTCCACCGAGGCCGCGCTTGAGGGATCTGAAGAGGTTCTAGAAGAGGGT  
 GTTCCCTCTTCGGGGTCCTCACCAAGAAGAGGTTCTGGGGTCGCCCTCTGAGGAGGCT  
 GC GG CTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCTGTAGTGATAATGTTG  
 GGAATAAGCTCTGCAACTTCTTGGCATTCA GTT G T T A A A A C A A A T A G G A T G C A A A T T C C  
 TCAACTCCAGGTTATGAAAACAGTACTTGGAAA ACTGAAA ACTACCTAAATG ATCGTCTTG  
 GTTGGGCCGTGTTCTTAGCGAGCAGAACGCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAG  
 CACATAGCCCACCTCCTAGGGACTGGAGGTGCCGCTACTACCATGGTAATT CCTGTATCTG  
 CCGAGATGACAGTGGAACAGATGACAGTGTGACACCCAACAGCAACAGGCCGAGAACAGTG  
 CAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCCCTGTCGGCCACCAAGGAGGGC  
 CGAGGACCTCATGAGCCAAGGAGAAAGAAACAAATGTGGATGGCTAGTGTGGACACACT  
 GGCAGTAATACGGACTCTGTAGATAAGTAAGTATCTGACTCACGGTCACCTCCAGTGGAAAT  
 GAAAAGTGTCTGCCCGAACCATGACTTTAGGACTCCTCAGTCCTTAGGACATACTCG  
 CCAAGCCTGTGCTCACAGGGCAAAGGAGAATATTTAATGCTCCGCTGATGGCAGAGTAAA  
 TGATAAGATTTGATGTTTGCTTGCTGTCACTACTTGTCTGGAAATGTCTAAATGTTTC  
 TGTAGCAGAAAACACGATAAAGCTATGATCTTATTAGAG

## **FIGURE 4**

MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ  
AENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKQNVVDGLVLDTLAVIRTLVDKO

**Signal peptide:**

amino acids 1-16

**Casein kinase II phosphorylation site.**

amino acids 22-26, 50-54, 113-117

**N-myristoylation site.**

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

## **FIGURE 5**

GGCAGGCGCTGTCCACCGGGGGCGTGGGAGTGAGGTACCAGATTCA  
GCCAGGCCTCTGTTCTCGGAATCCGGGTGCTGCGGATTGAGGTCCC  
GTTCTAACGGACTG  
CAAG**ATG**GAGGAAGGCGGGAACCTAGGAGGCCTGATTAAGATGGTCC  
CATCTACTGGTCTTGT  
CAGGTGCCTGGGCATGCAAATGTGGGTGACCTCGTCTCAGGCT  
CTCCTGCTTTCCGAAGC  
CTTCCCCGACATACCTCGGACTAGTGCA  
GAGCAA  
ACTCTTCCCCTACTTCCACATCTC  
CATGGGCTGTGCCTTCATCAACCTCTGCATCTGGCTTCACAGC  
ATGCTGGGCTCAGCTCA  
CATTCTGGGAGGCCAGCCAGCTTACCTGCTGTTCTGAGC  
CTTACGCTGGCCACTGTCAAC  
GCCCGCTGGCTGGAACCCCGCACACAGCTGCCATGTGGGCC  
CTGCAAACCGTGGAGAAGGA  
GCGAGGCCTGGGTGGGGAGGTACCAGGCAGCCACCAGGG  
TCCCGATCCCTACCGCCAGCTGC  
GAGAGAAGGACCCAAGTACAGTGCTCTCGCCAGA  
ATTCTCCGCTACCATGGGCTGTCC  
TCTCTTGCAATCTGGCTGCGTCTGAGCAATGGGCT  
CTGCTGCTGGCCTGCCCTGGA  
AATAAGGAGCCT**TAG**CATGGGCC  
CTGCATGCTAATAAA  
ATGCTTCTCAGAA  
ATGAAAAAAA  
AAAAAAAAAAAAA

## **FIGURE 6**

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56107
<subunit 1 of 1, 231 aa, 1 stop
<NX(S/T): 0
MEEGGNLGGGLIKMVHLLVLSGAWGMQMWWTFVSGFLLFRSLPRHTFGLVQSKLFPFYFHISM
GCAFINLCILASQHAWAQLTFWEASQLYLLFLSLLATVNARWLEPRTTAAMWALQTVEKER
GLGGEVPGSHQGPDPYRQLREKDPKYSALRQNFFRYHGLSSLCNLGCVLSNGLCLAGLALEIRSL
```

**Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 86-103, 60-75

**Casein kinase II phosphorylation site.**

amino acids 82-86

**Tyrosine kinase phosphorylation site.**

amino acids 144-151

**N-myristoylation site.**

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 54-65

**G-protein coupled receptors proteins.**

amino acids 44-85

## **FIGURE 7**

AATTAGTAACTCTTCTGAGGGAGGTACCTATCACACAGGGGGAAAA**ATG**CTCTTTGGGT  
GCTAGGCCTCCAATCCTCTGTGGTTCTGTGGACTCGTAAAGGAAA~~ACTAAAGATTGAAG~~  
ACATCACTGATAAGTACATTTTATCACTGGATGTGACTCGGGCTTGGAAACTTGGCAGCC  
AGAACCTTGATAAAAAGGGATTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAAC  
AGCTTAAAGGCAGAACCTCAGAGAGACTCGTACTGTGCTTCTGGATGTGACCGACCCAG  
AGAATGTCAAGAGGACTGCCAGTGGGTGAAGAACCAAGTTGGGAGAAAGGTCTCTGGGT  
CTGATCAATAATGCTGGTGTCCCGCGTGCTGGCTCCACTGACTGGCTGACACTAGAGGA  
CTACAGAGAACCTATTGAAGTGAACCTGTTGGACTCATCAGTGTGACACTAAATATGCTC  
CTTGTCAGAAAGCTCAAGGGAGAGTTATTAAATGTCAGTGGAAAGGTTCAATGACAGCTTAAG  
ATCGTTGGAGGGGGCTATACTCCATCAAATATGCACTGGAAAGGTTCAATGACAGCTTAAG  
ACGGGACATGAAAGCTTTGGTGTGCACGTCTCATGCATTGAACCAGGATTGTTCAAAACAA  
ACTTGGCAGATCCAGTAAAGGTATTGAAAAAAACTGCCATTGGAGCAGCTGTCTCCA  
GACATCAAACACAATATGGAGAAGGTTACATTGAAAAAAAGTCTAGACAAACTGAAAGGCAA  
TAAATCCTATGTGAACATGGACCTCTCCGGTGGTAGAGTGCATGGACCAACGCTTAACAA  
GTCTCTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAATTCTGGATACCTCTG  
TCTCACATGCCAGCAGCTTGCAAGACTTTATTGTTGAAACAGAAAGCAGAGCTGGCTAA  
TCCCAGGCAGTGT**TGA**CTCAGCTAACCAATGTCCTCCAGGCTATGAAATTGGCCGAT  
TTCAAGAACACATCTCCTTCAACCCCCATTCTTATCTGCTCCAACCTGGACTCATTAGA  
TCGTGCTTATTGGATTGCAAAAGGGAGTCCCACCATCGCTGGTGGTATCCAGGGTCCCTG  
CTCAAGTTCTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCCTGCCCTGT  
ATTTAGGCTTGCCTGCTGGTGTGATGTAAGGGAAATTGAAAGACTTGCCTTCAAAATG  
ATCTTACCGTGGCCTGCCCATGCTTATGGTCCCCAGCATTACAGTAACGTGAATGTT  
AAGTATCATCTCTTATCTAAATATTAAAGATAAGTCAACCCAAAAAA  
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## **FIGURE 8**

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56406
><subunit 1 of 1, 319 aa, 1 stop
><MW: 35227, pI: 8.97, NX(S/T): 3
MLFWVLGLLILCGFLWTRKGKLKIEDITDKYIFITGCDSGFGNLAARTFDKKGFHVIACLT
ESGSTALKAETSERLRTVLLDVTDPENVKRTAQWVKNQVGEKGLWGLINNAGVPGVLAPTDW
LTLEDYREPIEVNLFGLISVTLNMLPLVKKAQGRVINSSVGGRLAIVGGGYTPSKYAVEGF
NDSSLRRDMKAFGVHVSCTIEPGLFKTNLADPVKVIEKKLAIWEQLSPDIKQQYGEFYIEKSLD
KLKGNKSYVNMDLSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQK
AELANPKAV
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 136-152

**N-glycosylation sites.**

amino acids 161-163, 187-190 and 253-256

**Glycosaminoglycan attachment site.**

amino acids 39-42

**N-myristoylation sites.**

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

## **FIGURE 9**

GCGGGCTGTTGACGGCGCTGCG**ATGG**CTGCCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTT  
 CCTCTCAGTCGGACTCCTGACGCCGCCAGTGGCGGGGCCCTGGGCCGCTGCCACCACT  
 GTAGTCATGTACCCACCAGCCGCCGCGCCCTCATCGGGACTTCATCTCGGTGACGCTGAG  
 CTTGGCGAGAGCTATGACAACAGCAAGAGTGGCGGCCGCTCGTGCTGGAGGAATGGA  
 AGCAACTGTCGAGATTGCAAGCGGAATATGATTCTCTCCTGCCTTCTGCTTTCTGT  
 GGACTCCTCTTACATCAACTTGGCTGACCATTGGAAAGCTCTGGCTTTCAGGCTAGAGGA  
 AGAGCAGAAGATGAGGCCAGAAATTGCTGGGTTAAAACCAGCAAATCCACCCGCTTACCAAG  
 CTCCTCAGAAGGCCGACACCCTGAGAACTTACCTGAGATTTCGTACAGAACAGACAA  
 AGACACATCAGCGGGGACCCACCTCACCTGCAGATTAGACCCCCAAGCCAAGACCTGAAGGA  
 TGGGACCCAGGAGGAGGCCACAAAAAGGCAAGAAGGCCCTGTGGATCCCCGCCGAAGGAG  
 ATCCCGAGAGGACAGTCATCAGCTGGAGGGAGCGGTGATCGAGCCTGAGCAGGGCACCGAG  
 CTCCCTTAAGAAGAGCAGAAAGTGCCTCCACCAAGCCTCCCCTGCCACCGGCCAGGACACAGGG  
 CACACCAGTGCATCTGAACATCGCCAGAAGGGCTGATTGACGTCTCCTGCATGCATGGA  
 AAGGATAACCGCAAGTTGCATGGGCCATGACGAGCTGAAGCCTGTGTCCAGGTCTTCAGT  
 GAGTGGTTGGCCTCGGTCTCACACTGATCGACCGCTGGACACCATGTGGATCTGGGTCT  
 GAGGAAAGAATTGAGGAAGCCAGGAAGTGGGTGTCGAAGAAGTTACACTTTGAAAAGGACG  
 TGGACGTCAACCTGTTGAGAGCACGATCCGCATCCTGGGGGGCTCCTGAGTGCCTACAC  
 CTGCTGGGGACAGCCTCTTGAGGAAAGCTGAGGATTTGAAATCGGCTAATGCCTGC  
 CTTCAGAACACCATCCAAGATTCTTACTCGGATGTGAACATCGGTAUTGGAGTTGCCACC  
 CGCACGGTGGACCTCCGACAGCACTGTGGCGAGGTGACCAGCATTGAGCTGGAGTTCCGG  
 GAGCTCTCCGTCTCACAGGGATAAGAAGTTCAAGGAGGAGCTGGTGCCTGTTCAATACCCACAGCA  
 CATCCACGGCTGTCTGGGAAGAAGGATGGCTGGTGCCTGTTCAATACCCACAGCA  
 GCCTCTTACCCACCTGGCGTATTCACGCTGGCGCCAGGGCCGACAGCTACTATGAGTAC  
 CTGCTGAAGCAGTGGATCCAGGGCGGGAAAGCAGGAGACACAGCTGCTGGAAGACTACGTGGA  
 AGCCATCGAGGGTGTCAAGACGCACCTGCTGCCACTCCGAGCCCAGTAAGCTCACCTTG  
 TGGGGAGCTGCCACGGCGCTTCAGTGCCTGCAAGATGGACCACCTGGTGTCTCCTGCCA  
 GGGACGCTGGCTCTGGCGTCTACCACGGCCTGCCAGCCACATGGAGCTGGCCCAGGA  
 GCTCATGGAGACTTGTACCAAGATGAACCGGCAGATGGAGACGGGCTGAGTCCCAGATCG  
 TGCACTTCAACCTTACCCCCAGCCGGCGTCTGGACGTGGAGGTCAAGCCAGCAGACAGG  
 CACAACCTGCTGCCAGAGACCGTGGAGAGCCTGTTACCTGTACCGCGTCACAGGGGA  
 CCGCAAATACCAGGACTGGGCTGGAGATTCTGCAGAGCTCAGCCATTCAACACGGGCC  
 CCTCGGGTGGCTATTCTCATCAACATGTCCAGGATCCTCAGAAGCCGAGCCTAGGGAC  
 AAGATGGAGAGCTTCTTCTGGGGAGACGCTCAAGTATCTGTTCTGCTCTCCGATGA  
 CCCAAACCTGCTCAGCCTGGACGCCACGTGTTCAACACCGAAGCCCACCCCTGCTTCA  
 GGACCCCTGCC**TAG**GGTGGATGGCTGCTGGTGTGGGACTTCGGGTGGCAGAGGCACCTTG  
 CTGGGTCTGGCATTTCAGGGCCACGTAGCACCAGCAACCGCAAGTGGCCAGGGCT  
 CTGAACCTGGCTCTGGCTCTCGTCTGCTTAACTCAGGACACCGTGAGGACAAGTGA  
 GGCGTCAGTCTGGTGTATGGGGCTGGGCCGCTGGAGCCTCCGCCCTGCTTCTC  
 CAGAACACGAATCATGACTCACGATTGCTGAAGCCTGAGCAGGTCTCTGTGGGCCAGCA  
 GAGGGGGCTCGAGGGTGGTCCCTGGTACTGGGGTGACCGAGTGAGCAGCCCAGGGTGCAGC  
 TCTGCCCGGCTCGTAAGCCTCAGATGTCCCCAATCCAAGGGCTGGAGGGCTGCCGTGA  
 CTCCAGAGGCCTGAGGCTCCAGGGCTGGCTCTGGTGTGTTACAAGCTGGACTCAGGGATCCTC  
 CTGGCCGCCCGCAGGGGCTTGGAGGGCTGGACGGCAAGTCCGTCTAGCTCACGGGCC  
 CCAGTGGAAATGGGTCTTCGGTGGAGATAAAAGTTGATTGCTTAACCGCAA

## **FIGURE 10**

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><subunit 1 of 1, 699 aa, 1 stop
><MW: 79553, pI: 7.83, NX(S/T): 0
MAACEGRRSGALGSSQSDFLTPVGGAPWAVATTVVMYPPPPPPHRDFISVTLSFGESYDN
SKSWRRRSCWRKWKQLSRLQRNMILFLLFCGLLFYINLADHWKALAFRLEEEQKMRPE
IAGLK PANPPVLPAPQKADTDPENLPEISSQKTQRHIQRGPPHLQIRPPSQDLKDGTQEEAT
KRQEAPVDPRPEGDPQRTVISWRGA VIEPEQGT ELP SRAEVPTK PPLP PART QGTPVHLNY
RQKGVIDVFLHAWKG YRKFAWGHDELKPVSRSFSEWFG LGLTLIDALDTM WILGLRKEFEEA
RKWVSKKLHFEKDVDVNL FESTIRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKI
PYSDVNIGTGVAHPPRWTSDSTVAEVTSIQLEFRELSRLTGDKKFQEAVEKVTQHIHGLSGK
KDGLVPMFINTHSGLFTHLGVFTL GARADSYYEYLLKQWIQGGKQETQLLEDYVEAIEGVRT
HLLRHSEPSKLT FVGELAHGRFSAKMDHLCFLPGTLALGVYHGLPASHMELAQELMETCYQ
MNRQMETGLSPEIVHFNLYPQPGRRDVEVKPADRHNL RPETVESLFYLYRVTGDRKYQDWG
WEILQSFSRFTRVPSSGYSSINNVQDPQKPEPRDKMESFFLGETIKYLFL FSDDPNLLSLD
AYVFNTEAHPLPIWTPA
```

**Important features of the protein:**

**Transmembrane domain:**

amino acids 21-40 and 84-105 (type II)

## **FIGURE 11**

GGCGCCGCGTAGGCCGGAGGCCGGCCGGCTGCGAGCGCCTGCCCATGCGCCGC  
 CGCCTCTCCGCACG**ATG**TTCCCCTCGCGAGGAAAGCGCGCAGCTGCCCTGGGAGGAACGGC  
 AGGTCCGGGTTGCTCTCCGGCGCTCCCTCGGAAGTGTTCGTCTTCCACCTGTTCGTGGC  
 CTGCCTCTCGCTGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGACGTGG  
 CCCGGCAGTCAGGGACAAGGGCAGGAGACCTCGGGCCCTCCCCGTGCCTGCCCTGGCAGAG  
 CCGCCCCCTGAGCACTGGGAAGAAGACGCATCCTGGGGCCCCACCGCCTGGCAGTGCTGGT  
 GCCCTCCGCGAACGCTCGAGGAGCTCCTGGCTTCGTGCCACATGCGCCGCTCCTGA  
 GCAGGAAGAAGATCCGGCACCATCTACGTGCTCAACCAGGTGGACCACCTCAGGTTAAC  
 CGGGCAGCGCTCATCAACGTGGCTTCCTGGAGAGCAGAACAGCACGGACTACATTGCCAT  
 GCACGACGTTGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTCGTAGGGCTGGC  
 CCTTCCACGTGGCCTCCCCGGAGCTCCACCCCTCTACCAACTACAAGACCTATGTCGGCGGC  
 ATCCTGCTGCTCTCCAAGCAGCACTACCGGCTGTGCAATGGGATGTCCAACCGCTCTGGG  
 CTGGGCCGCGAGGACGAGTTCTACCGCGCATTAAAGGGAGCTGGCTCCAGCTTTCC  
 GCCCTCGGAATACAACACTGGTACAAGACATTGCCACCTGCATGACCCAGCCTGGCGG  
 AAGAGGGACCAGAAGCGCATCGCAGCTAAAAACAGGAGCAGTTCAAGGTGGACAGGGAGGG  
 AGGCCTGAACACTGTGAAGTACCATGTGGCTCCCGACTGCCCTGTCTGTGGCGGGGCC  
 CCTGCACTGTCCTAACATCATGTTGGACTGTGACAAGACGCCACACCCCTGGTGCACATT  
**AGCTGA**GCTGGATGGACAGTGAGGAAGCCTGTACCTACAGGCCATTGCTCAGGCTCAGGA  
 CAAGGCCTCAGGTCGTGGCCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCA  
 AGCTACGCAATTGCAGCCACCCGGGCCAAGGCAGGCTTGGCTGGCCAGGACACGTGGG  
 GTGCCCTGGGACGCTGCTGCCATGCACAGTGATCAGAGAGAGGCTGGGTGTCCCTGTCCG  
 GGACCCCCCTGCCTCCTGCTCACCTACTCTGACCTCCTCACGTGCCAGGCCTGTGG  
 TAGTGGGAGGGCTGAACAGGACAACCTCTCATCACCTACTCTGACCTCCTCACGTGCC  
 AGGCCTGTGGGTAGTGGGGAGGGCTGAACAGGACAACCTCTCATCACCCCCAAAAAAA  
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## **FIGURE 12**

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56531
><subunit 1 of 1, 327 aa, 1 stop
><MW: 37406, pI: 9.30, NX(S/T): 1
MFPSRRKAAQLPWEDGRSGLLSGGLPRKCSVFHLVACLSLGFFSLLWLQLSCSGDVARAVR
GQQQETSGPPRACPPEPPPEHWEEDASWGPRLAVLVPFRERFEELLVFVPHMRRFLSRKKI
RHIIYVLNQVDHFRFNRAALINVGFLESSNSTDYIAMHDV DLLPLNEELDYGFPEAGPFHVA
SPELHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDDDEFYRRIKGAGLQLFRPSGI
TTGYKTFRHLHDPAWRKRDQKRIAAQKQEQFKVDREGGLNTVKYHVASRTALSVGGAPCTVL
NIMLDCKTATPWCTFS
```

**Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 29-49 (type II)

**N-glycosylation site.**

amino acids 154-158

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 27-31

**Tyrosine kinase phosphorylation site.**

amino acids 226-233

**N-myristoylation site.**

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

**FIGURE 13**

CAATGTTGCCTATCCACCTCCCCAAGCCCCTTACCT**ATG**GCTGCTGCTAACGCTGCTGCT  
GCTGCTGCTGCTGCTAAAGGCTCATGCTTGGAGTGGGACTGGTCGGTGCCAGAAAGTCT  
CTTCTGCCACTGACGCCCATCAGGGATTGGCCTTCTTCCCCCTCCCTTCTGTGTCTC  
CTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGAAGGGGAGAAAGT  
GGGGGATGGC**TAA**GAAAGCTGGAGATAGGAACAGAACAGGGTAGTGGGTGGCTAGGGGG  
GCTGCCTTATTAAAGTGGTGTTATGATTCTTATACTAATTATAACAAAGATATTAAGGC  
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AAATATGTCTTATAATAACAGTTAAAGCTGAAAAAAAAAAAAAAA

## **FIGURE 14**

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56862
<subunit 1 of 1, 73 aa, 1 stop
<MW: 7879, pI: 7.21, NX(S/T): 0
MLLLTLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCQAO
PRGEGEKVGDG
```

**Important features:**

**Signal peptide:**

amino acids 1-15

**Growth factor and cytokines receptors family:**

amino acids 3-18

## **FIGURE 15**

GGGACCCATGCGGCCGTGACCCCCGGCTCCCTAGAGGCCAGCGCAGCCGAGCGGACAAAG  
 GAGCATGTCCGCGCCGGGAAGGCCGTCCTCCGGCCATAAGGCTCCGGTCGCCGCTGG  
 GCCCGCGCCCGCCTGCCGCCGGCTCCGGGCCGCTAGGCCAGTGCGCCGCCG  
 CTCGCCCGCAGGCCGGCCGCAGCATGGAGGCCACCCGGACGCCGGCGGGGCCGCGCA  
 GCCGCCGCTGTTGCTGCCGCTCGCTGTTAGCGCTGCTCGCCTGCTGGGAGGCGGCG  
 GCGCGGCCGCCGCGCTGCCGCCGGCTCAAGCACCGATGGCGGCCGGAGGGCTGGC  
 AGGGCGGCCGGCGCCGCCGAGGGCAAGGTGGTGTGCAGCAGCCTGGAACTCGCGCAGGTCC  
 GCCCCCAGATACTCTGCCAACCGCACGGTACCCCTGATTCTGAGTAACAATAAGATATCCG  
 AGCTGAAGAATGGCTCATTCTGGGTTAAGTCTCCTGAAAGATTGGACCTCGAAACAAT  
 CTTATTAGTAGTATAGATCCAGGTGCCTCTGGGACTGTCATCTCTAAAAAGATTGGATCT  
 GACAAACAATCGAATAGGATGTCTGAATGCAGACATATTGAGGACTACCAATCTGGTTC  
 GGCTAAACCTTCGGGAAATTGTTCTCATTATCTCAAGGAACCTTGATTATCTTGC  
 TCATTACGGTCTTGGAAATTCCAGACTGAGTATCTTTGTGTGACTGTAACATACTGTGGAT  
 GCATCGCTGGTAAAGGAGAAGAACATCACGGTACGGGATACCAGGTGTGTTATCCTAAGT  
 CACTGCAGGCCAACCAACCAGTCACAGCGTGAAGCAGGAGCTGTTGACATGCGACCCCTCCGCT  
 GAATTGCCGTCTTCTACATGACTCCATCTCATGCCAACGTTGTGTTGAAGGAGACAGCCT  
 TCCCTTCCAGTGCATGGCTCATATATTGATCAGGACATGCAAGTGTGTTGATCAGGATG  
 GGAGAATAGTTGAAACCGATGAATCGCAAGGTATTTGTTGAAAAGAACATGATTCAAAC  
 TGCTCCTGATTGCAAGTGCCTAACCATTTCTAATATTGAGGCTGGATCTACTGAAATTG  
 GGGCTGTATGTCCAGACCAACGTGGAAATAACGAGGACTGTGGATATTGTGGTATTAG  
 AGAGTTCTGCACAGTACTGTCCTCCAGAGAGGGTGGTAAACAACAAAGGTGACTTCAGATGG  
 CCCAGAACATTGGCAGGCATTACTGCATATCTCAGTGTACCGGAACACCCATGGCAGTGG  
 GATATATCCGGAAACCCACAGGATGAGAGAAAAGCTGGCGCAGATGTGATAGAGGTGGCT  
 TTTGGCAGATGATGATTATTCTCGCTGTCAGTATGCAAATGATGTCAGTAGAGTTCTTAT  
 ATGTTAACATCAGATGCCCTCAATCTACCAATGCCGTGGCAACAGCTGACAGTTACTGGC  
 TTACACTGTGGAAGCAGCCAACCTTCTGACAAAATGGATGTTATTTGTCAGGAAATGA  
 TTGAAAATTGGAAAGATTACCAAGGGAGAAAATCAAAGAGCTAGGTGACGTGATGGTT  
 GACATTGCAAGTAACATCATGTTGGCTGATGAAACGTGTCCTGTGGCTGGCAGAGGGAAAGC  
 TAAAGCCTGCAGTAGGATTGTCAGTGTCTTCAGCGATTGCTACCTACCGGCTAGCCGGTG  
 GAGCTCACGTTATTCAACATATTACCCAATTGCTCTGGAAGCTTATGTCATCAAGTCT  
 ACTGGCTCACGGGATGACCTGTCAGGAAAGTGGCAGCCTCTGATCGTACAGG  
 ACTTCGGATTATGGAGGCGGGATCCAGAGGGAAACCTGGATAAGCAGCTGAGCTTAAGT  
 GCAATGTTCAAATACATTTCAGTCTGGCACTAAAGGTATGTTACATTCTGCAATCATTT  
 AAGACTATTACAGTTAAATTAGAATGCTCAAATGTTCTGCTCGAAAATAACCTTATTA  
 AAAGATTTTTTGCAAGGAAGATAGGTATTATTGCTTTGCTACTGTTAAAGAAAAC  
 ACCAGGAAGAACTGCATTACGACTTCAAGGGCCCTAGGCATTGCTTGCCTTGATTCCCTT  
 CTTCACATAAAATACAGAAATTACATTATACTGCACTGGTATAATGCAAATATACT  
 ATTGTTACATGTGAAAAATTGACTTAAAGTTATTGTTATTGTTTTGCTCCT  
 GATTTAAGACAATAAGATGTTCATGGGCCCTAAAGTATCATGAGCCTTGGCACTGC  
 GCCTGCCAACGCTAGTGGAGAAGTCACCCCTGAGACCAGGTGTTAATCAAGCAAGCTGTAT  
 ATCAAAATTGGCAGAAAACAAATATGTCATATATCTTTTAAAGTATTCA  
 TTGAAGCAAGCAAATGAAAGCATTGACTGATTAAAATTGGTGTCTTAGATATATT  
 GACTACACTGTATTGAAGCAAATAGAGGGAGGCACAACCTCCAGCACCCCTAATGGAACCACATT  
 TTTTCACTTAGCTTCTGTGGCATGTGTAATTGTTAGTCTGCGGTTTAATCTCACAG  
 TACTTATTCTGTCTGTCCTCAATAATACAAACAATATTCCAGTCATTAAATGGC  
 TGCATAATAACTGATCCAACAGGTGTTAGGTGTTAGTGTGAGCACTCAATAAATA  
 TTGAATGAATGAACGAAAAAAAAAAAAAA

## **FIGURE 16**

MEPPGRRRGRAQPPLLPLSLLALLALLGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK  
VVCSSLELAQVLPPDTLPNRTVTLLSNNKISELKNGSFSGLSLLERLDLRNNLISSIDPGA  
FWGLSSLKRDLTNNRIGCLNADIFRGLTNLVRLNLSGNLFSSLSQGTFDYLASLRSLEFQT  
EYLLCDCNILWMHRWVKEKNITVRDTRCVYPKSLQAQPVTGVKQELLCDPPELPSFYMTP  
SHRQVVFEGDSLFPQCMASYIDQDMQVLWYQDGRISETDESQGI FVEKNMIHNCSLIASALT  
ISNIQAGSTGNWGCHVQTKRGNNRTVDIVVLESSAQYCPPERVVNNKGDFRWPRLAGITA  
YLQCTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDYSRCQYANDVTRVLYMFNQMPLNL  
TNAVATARQLLAYTVEAANFSDKMDVIFVAEMIEKFGRTKEKSKELGDVMDIASNIMLA  
DERVLWLAQREAKACSRIVQCLQRIATYRLAGGAHVYSTYSPNIALEAYVIKSTGFTGMTCT  
VFQKVAASDRTGLSDYGRRDPEGNLDKQLSFKCNVSNTFSSLALKVCYILQSFKTIYS

**Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 13-40 (type II)

**N-glycosylation site.**

amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336,  
433-437, 453-457, 592-596

**N-myristoylation site.**

amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57,  
57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326,  
384-390, 403-409, 554-560

**FIGURE 17**

GCGTGGGGATGTCTAGGAGCTCGAAGGTGGTGCCTGGCCTCTCGTGCTGCTGACGGCGGCC  
ACAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTCGTGACGGAGTTAT  
CAGAGACATTGAGAGGCAAATTGGAAAAAGAAAACATTGTCCTTGGGAGAACAGATTA  
TTTGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATTTATTGGCAAAAGGATCTAAAAAA  
**TCATGACTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTGTGTGTGTTGATCA**  
GGAGAGTAGCTTAGTATCTTCATCTTTGGTCACTGTCCTTTAAACTGATCA  
AATAAAGGACAGTGGTCATATAAGTTACTGCTTCAGGGTCCCTATATCTGAATAAAGGA  
GTGTGGGCAGACACTTTGGAAGAGTCTGTCGGGTGATCCTGGTAGAAGCCCCATTAGGG  
TCACTGTCCAGTGCTTAGGGTTGTTACTGAGAACACTGCCGAGCTTGTGAGAAGGAAGGGA  
TGGATAGTAGCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACAC  
TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTCGAATCC

## **FIGURE 18**

MSRSSKVVLGLSVLLTAATVAGVHVKKQQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT  
EQLEAEREKMLLAKGSQKS

**Signal peptide:**

amino acids 1-21

## **FIGURE 19**

CTGTCGTCTTGCTTCAGCCGCAGTCGCCACTGGCTGCCTGAGGTGCTCTTACAGCCTGTC  
CAAGTGTGGCTTAATCCGTCTCCACCACCAAGATCTTCTCCGTGGATTCCCTCTGCTAAGACC  
GCTGCC**ATG**CCAGTGACGGTAACCGCACCACCATCACAAACCACCGACGTATCTTCGGG  
CCTGGGGTCCCCATGATCGTGGGTCCCCTGGGCCCTGACACAGCCCTGGTCTCCTCGC  
CTGCTGCAGCTGGTGTACCTGCCTGGCTTCTCGCTGGTGGCTAGCGTGGCGCTGGAC  
GGGGTCCATGGGCAACTGGTCCATGTTCACCTGGTCTGCTTCTCCGTGACCCTGATCA  
TCCTCATCGTGGAGCTGTGCAGGCTCCAGGCCGCTTCCCTGTCTGGCGCAACTTCCC  
ATCACCTCGCCTGCTATGCAGGCCCTCTGCCTCTGCCATCATCTACCCACAC  
CTATGTCCAGTCCCTGTCCCACGGCGTTCGCAGGACACGCCATGCCGCCACCTTCTTCT  
CCTGCATCGCGTGTGGCTTACGCCACCGAACGGCTGCTGAAGGTGCTGGAGACCTCGTGCCTG  
CATCATCTTCGCGTTCATCAGCGACCCAAACCTGTACCAAGCACCAGCCGGCCCTGGAGTG  
GCGTGGCGGTGTACGCCATCTGCTTACCTAGCGGCCATGCCATCCTGCTGAACCTGGGG  
GAGTGCACCAACGTGCTACCCATCCCCTCCCCAGCTTCTGTCGGGCTGGCTTGCTGTC  
TGTCCCTCTATGCCACCGCCCTGTTCTCTGGCCCTCTACAGTCATGAGAAGTATG  
GCGGCCAGCCTCGCGCTCGAGAGATGTAAGCTGCAGCCGAGCCATGCCACTACGTGT  
GCCCTGGACCAGCGACTGGCTGTGGCATCCTGACGCCATCAACCTACTGGCGTATGTGG  
TGACCTGGTGCACTCTGCCACCTGGTTTGTCAGGTCTAA**TAA**GACTCTCCAAGAGGCTCC  
CGTCCCTCTCCAACCTTTGTTCTTCTGCCAGTTCTTATGGAGTACTTCTTCC  
TCCGCCTTCCCTGTTCTCTGCTCCCTGCTCTCCCTCCACCTTTCTTCCCTGCTGT  
CAATTCTTGCACTCTAACAGTTCTGGATGCATCTTCTCCCTTCCCTGCTGT  
TTCTTCTGTTGTTGCCACATCCTGTTTCAACCTGAGCTGTTCTCTTCTTCTTCTTCT  
CTTTCTTCTTTTTTTTTTAAGACGGATTCTCACTCTGTCGCCAGGCTGGAG  
TGCAGTGGTGCATCTCAGCTCACTGCAACCCCGCCTGGTTCAAGCGATTCTCC  
CCCAGCCTCCAAAGTAGCTGGGAGGACAGGTGTGAGCTGCCGCACCCAGCCTGTTCTT  
TTCCACTCTTTCTCATCTTCTGGGTGCCTGCGCTTCTTATCTGCC  
TTTGCAAGCACCTCTGTCCTGGGAGCCCTGAGACTTCTTCTCCCTGCC  
CCCACCTCCAAAGGTGCTGAGCTCACATCCACACCCCTGCAAGCGTCCATGCC  
CCAAGGGGCCATTGCCAAAGCATGCCCTGCCACCCCTCGCTGTCCTAGTCAGTGT  
GTGTGTGTGTGTGTTGGGGGTGGGGTAGCTGGGATTGGCCCTTCTTCT  
CCCAGTGGAGGAAGGTGTGCAGTGTACTTCCCTTAAATTAAAAACATATATATAT  
ATTGGAGGTCACTAATTCCAATGGCGGGAGGCATTAAGCACCACCTGGTCC  
CCCCGCCTGGCACTCAGCCTGCCAGAGATTGGCTCCAGAATTGGCCAGGCTACAGAACAC  
CCACTGCCCTAGAGGCCATCTAAAGGAAGCAGGGCTGGATGCCTTCACTCC  
CTGTGGTATGAAAAAG

## **FIGURE 20**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727
<subunit 1 of 1, 322 aa, 1 stop
<MW: 35274, pI: 8.57, NX(S/T): 1
MPVTVTRTTITTTTSSSGLSPMIVGSPRALTQPLGLRLLQLVSTCVAFSLVASVGAWTG
SMGNWSMFTWCFCFSVTЛИLIVELCGLQARFPLSWRNFPITFACYAALFCLSASIYPTTY
VQFLSHGRSRDHAIATFFSCIACVAYATEVAWTRARPGEITGYMATVPGLLKVLETFVACI
IFAFISDPNLYQHQPALEWCVAVYAICFILAAIAILLNLGECTNVLPPIPFPSSFLSGLALLSV
LLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRRLAVAILTAINLLAYVAD
LVHSAHLVFKV
```

**Important features:**

**Transmembrane domains:**

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192,  
205-226, 235-255 and 294-312

**N-glycosylation site.**

amino acids 66-69

**Glycosaminoglycan attachment site.**

amino acids 18-21

## FIGURE 21

GAACGTGCCACCATGCCAGCTAATTGGTATTTAGTAGAGACGGGTTTACCATGTTGCCAGGCTGGTC  
 TTGAACCTCGTACCTCATGATCGCTCACCTCGGCCTCCAAAGTGTGGATTACAGGCATGACCAACTGACGC  
 CTGCCAGCCTATGCATTAAAGAAATTATTCTGTATTAGTGCTGTGCTAAACATTGGCACTACAGTGACCA  
 AAACAGACTGAATTCCCCAAGAGCAAAGACCAAGGAGACCAACAAGAAACAGGAATGCAAAAGAGACCA  
 TTATTACTCACTATGACTAAGGTACAATGGGTACGGTATGGAGAGTGTGTTAAGAGACTACAGAGGG  
 AGGACAGACTACCAAGAGGGGCCAGGAAAGCTCCTGACGAGGTGGTATTCAAGCCAAACTGGAAGAATGA  
 GAAAGAGCTAGCCAGCCATCAGAATAGTCCAGAAGAGATGGGAGCACTACACTACACTTTGGCCTGAGAA  
 AATAGCATGGGATTGGAGGAGCTGGGGAACACCACTCTGCCGACCTGGGCAGGAGGCATTGAGGGCTTGAGA  
 AAGGGCAATGGCAGTAGCAGTAGAAAGGACAGGGTAGGAGCAGGGACTTGCAGGTGGAAATCATTAGGTCTTATC  
 AACAGATATGGCAAGCAAAGCCAGGGAGAATTGATGGTAATGCTGAGGTTGGAGGCCAGGCTAGATGGACAG  
 TGGTGGGTGATGCAAAGGAAAGAGGTCAAGGAAGCAGGGCAGACGTGGGAGAAGGTGTGGGGTTGGTTCCA  
 TCTTGCAGTCTGCCGAATGTGGATGGGAAGACCAAGAGGAGGAGCAAGGGCAGAGGGAAAGGGAAATCTTAA  
 AGAAGTCCTGGATGCCACACTCTTCTCTCTCCCTCAGAGGTCTCACTCGTGGTCTTCA  
 TTCCTGCCCTGCCTCCATCTCCTCTGGGTGCTGGAAAGTGGAGGATTAGCTGAAGTTTGCTTCTCGGGGCTG  
 TCTGAATCTCATTGCTTCTGGGAGGACATAATTACCTGTCTAGCTTCTATCATCTTACATTCCCTGTAG  
 CCACTGGGACATATGTGGTCTCTAGCTCTGTCTCCTCATGCCCTTGCTGGGTATGGCATGTTAG  
 GGGGAAGGTATTGCTGTCAGAGGGCACTGACTTTCTAATGGTGTACCCAAGGTGAATGTTGGAGACACAGTC  
 GCGATGCTGCCAAGTCCCGCGAGCCCTAATCCAGGAGATCGTGCCTGCCAGGTCCCTGCGATGGT  
 ATGCAGCCCCCTCCC**AT**GTTCTGGCCTTGTCTCCCTCCGTTGCACATCCCTTGGAACTGTTCT  
 GTGAGTACATGCTGGGTCTCCCCCTTCTCCCTTGCTCAGGTGAATCTCAGGCCCTCTCCCACCCAAAGGTTC  
 ACATGGATCCTAACTACTGCCACCCCTCCACCTCCCTGCACTGTGCTCCCTGCCCTGGTCTTACCCAGGCTTC  
 TCCACCTCCCTATCTCAGGTATTCCCAGGTGGAGGACCGACGTGACCAAGCCTACGCCATGGCCAGG  
 GCCGAGTGGCTCACCTCATTGAGTGGAGGGCTGGAGCAAGCCGAGTGACTIONCCTGCTGCCCTGGAATCAGCCT  
 TTCCCTCATTACAGACCTCAGCGAGGGAGAACAAGAGGCTCGCTTGCAGCAGGAGTGGCTGAGCAGTTGCCA  
 TCGCGGAAGCCAAGCTCCGAGCATGGTCTCAGGTGGATGGCGAGGACTCCACTGATGACTCTATGATGAGGACT  
 TTGCTGGGGGAATGGACACAGACATGGCTGGCAGCTGCCCTGGGCCGACCTCCAGGACCTGTTACCGGCC  
 ACCGGTTCTCCGGCTGTGCGCCAGGGCTCGTGGAGCCTGAGAGCGACTGCTCACAGACCGTGTCCCCAGACA  
 CCCTGTGCTCTAGTCTGTCAGCCTGGAGGATGGGTGTTGGCTCCCCGGCCGGCTGGCTCCCAGCTGCTGG  
 GCGATGAGCTGCTCTGCCAAACTGCCCCCAGCCGGAAAGTGCCTTCCGAGCTGGCCACTGGAGGCCCC  
 AGGACTCACTACAACTGCCCTCACAGAGTCCTGCCCTCCCCGGGGAGGAGGCCAGCCCCCTCCAAGG  
 ACTGCCAGCCACTCTGCCACCCTAACGGCAGCTGGGAACGGCAGCGGCAAGCCTGACCTGCCCTTCT  
 GGGTGGTGTCTTAGATGAGGATGAGGCAGAGCCAGAGGAACAG**TGA**CCCACATCATGCCCTGGCAGTGGCATGCA  
 TCCCCGGCTGCTGCCAGGGCAGAGCCTCTGTGCCCAAGTGTGGCTCAAGGCTCCAGCAGAGCTCCACAGCC  
 TAGAGGGCTCTGGGAGCGCTGCTCTCCGTGTTGCTGTTGCTGATGAAAGTGTGTTGGAGAGGAGGCAGGGCTG  
 GGCTGGGGGCCATGTCTGCCCTCCCTCCGGCTTGGCGGGGGTGGCCGGGGCTCTGGGCATGGCTACA  
 GCTGTGGCAGACAGTGATGTTCATGTTCTAAATGCCACACACATTTCTCTCGGATAATGTGAACCACTA  
 AGGGGTTGTGACTGGGCTGTGAGGGTGGGGAGGGGCCAGCAACCCCCCACCCTCCATGCCCTCTC  
 TCTTCTGCTTTCTCTCACTTCCGACTCCATGTGCACTGCTGTTGATAGAATACCCCCCACCCTGGAGGGCTG  
 CTCTGCCCTCCCGAGCCTATGGGTGAGCCGTCCTCAAGGGCCCTGCCAGCTGGCTCGTGTGCTTC  
 ATTACACTCTCATGTCCTAAATCTCTTTCTAAAGACAGAAGGTTTTGGCTGTTCTCAGTC  
 GGATCTCTCTCTGGGAGGCTTGGAAATGATGAAACATGACCTCCACCCCTTCTGGCCCCCTAAATGG  
 GGCTGGGCCCTTCCAAACCCCTCTAGGATGTGCGGCAGTGTGCTGGCGCTCACAGCCAGCCGGCTGCC  
 ATTACAGCAGAGCTCTGAGCGGGAGGTGGAGAAGAAAGGATGGCTGGTTGCCACAGAGCTGGACTCATGTT  
 CTTCTAGAGAGGGCCACAGAGGGCAGGGGTGGCCGGAGTTGTCAGCTGATGCCCTGCTGAGAGGCAGGAAT  
 TGTGCCAGTGAGTGACAGTCATGAGGGAGTGTCTCTGGGAGGAAAGAAGGTAGAGCCTTCTGCTGAAT  
 GAAAGGCCAGGCTACAGTACAGGGCCCGCCAGCCAGGGTGTAAATGCCACGTAGTGGAGGCCTGGCAG  
 ATCTGCATTCCAAGGTCACTGGACTGTACGTTTATGGTTGTGGAGGGTGGCTTGAATAAGGGC  
 CTTGAGGCTTGGCAGGTAAGAGGGCCAAGGTAAGAACGAGGCCAACGGCACAAGCATTCTATATAAGT  
 GGCTCATTAGGTGTTATTTGTTCTATTAAAGAATTGTTTATTAAATAAATAAAACTTGTAAATCTC  
 TAAAA

## **FIGURE 22**

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSSLAQVNLSFPSHPKVHMDPNYCHPSTSLHLCS  
LAWSFTRLLHPPPLSPGISQVVKDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPALESAFSSY  
SDLSEGEQELEARFAAGVAEQFAIAEAKLRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLG  
PHLQDLFTGHRFSRPVRQGSVEPESDCSQTVPDTLCSSLCSLEDGLLGSPARLASQLLGDE  
LLLAKLPPSRESAFRSLGPLEAQDSLYNSPLTESCLSPAEEEPAPCKDCQPLCPPLTGSWER  
QRQASDLASSGVVSLDEDEAEPEEQ

**Signal peptide:**

amino acids 1-15

**Casein kinase II phosphorylation site.**

amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232,  
285-289, 324-328

**Tyrosine kinase phosphorylation site.**

amino acids 44-52

**N-myristoylation site.**

amino acids 17-23, 26-32, 173-179

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 11-22

## **FIGURE 23**

GGTCCTGGCGCTGTTACACAAGCAAGATAACGCCAGCCCCACCTAATTTGTTCCCT  
 GGCACCCTCCTGCTCAGTGCACATTGTACACTTAACCCATCTGTTCTCTAATGCACGA  
 CAGATTCCCTTCAGACAGGACAACGTGATATTCAAGTTCAGTTCTGATTGTAAATACCTCCTAAG  
 CCTGAAGCTCTGTTACTAGCCATTGTGAGCTCAGTTCTCATCTGCAAAATGGGCATAA  
 TACAATCTATTCTGCCACATCAAGGGATTGTTATTCCCTTAAAAAAACCAATACCAAAG  
 AAGCCTACAATGTTGGCCTAGCCAAAATTCTGTTGATTCAACGTTGTTTATTCACTTCT  
 ATCGGGGAGCCATGGAAAAGAAAATCAAGACATAAACACACAGAACATTGCAGAAGTT  
 TTAAAACAATGGAAAATAAACCTATTCTTGAAAGTGAAGCAAACCTAAACTCAGATAAA  
 GAAAATATAACCACCTCAAATCTCAAGGCGAGTCATTCCCCTCCTTGAATCTACCCAA  
 CAGCCACGGAATAACAGATTCTCCAGTAACTCATCAGCAGAGCATTCTGGCAGTCTAA  
 AACCCACATCTACCATTCCACAAGCCCTCCCTGATCCATAGCTTGTCTAAAGTGCCT  
 TGGAATGCACCTATAGCAGATGAAGATCTTGCCTCTCAGCACATCCAATGCTACACC  
 TGCTCTGTCTCAGAAAACCTCACTGGTCTTGGTCAATGACACCGTGAAAACCTCTGATA  
 ACAGTCCATTACAGTTAGCATCCTCTTCAGAACCAACTCTCCATCTGTGACCCCTTG  
 ATAGTGGAACCAAGTGGATGGCTTACCAACAGTGTAGCTACTGGTTACCCCTTA  
 TCAAGAAAAACAACTCTACAGCCTACCTTAAATTCCAATAATTCAAACACTCTTCAA  
 ATACGTAGATCCCCAAAAGAAAATAGAAATACAGGAATAGTATTGGGCCATTTAGGT  
 GCTATTCTGGGTGTCCTTGCTACTCTGTGGCTACTTGTGTGGAAAAAGGAAAC  
 GGATTCAATTCCCCTCGGCAGTTATGACGACAGAAATGAACCAGTTCTGCGATTAGACA  
 ATGCACCGAACCTTATGATGTGAGTTGGAAATTCTAGCTACTACAATCAAACCTTGAAT  
 GATTCAAGCCATGCCAGAAAGTGAAGAAAATGCACGTGATGGCATTCTATGGATGACATA  
 TCCACTTCGTACTTCTGTATAGAACTAACAGCAAAAGCGTTAACAGCAAGTGTCTA  
 CATCCTAGCCTTGTACAATTCTTCAAAAGGTACACAAATTACTGTACGTGGAT  
 TTTGTCAAGGAGAATCATAAAAGCAGGAGACCGAGTAGCAGAAATGTAGACAGGATGTATCAT  
 CCAAAGGTTTCTTACAATTGGCATCCTGAGGCATTACTAAGTAGCCTTAATT  
 TGTATTAGTAGTATTCTTAGTAGAAAATATTGTGGAAATCAGATAAAACTAAAAGATT  
 TCACCAATTACAGCCCTGCCTCATAACTAAATAAAAATTATTCCACCAAAATTCTAAA  
 ACAATGAAGATGACTCTTACTGCTCTGCCTGAAGCCCTAGTACCATATTCAAGATTGCAT  
 TTTCTTAAATGAAAATTGAAAGGGTGTGTTAAAGAAAATTGACTAAAGCTAAAAGAG  
 GACATAGCCCAGAGTTCTGTTATTGGAAATTGAGGCAATAGAAATGACAGACCTGTATT  
 TAGTACGTTATAATTCTAGATCAGCACACACATGATCAGCCACTGAGTTATGAAGCTGA  
 CAATGACTGCATTCAACGGGCCATGGCAGGAAAGCTGACCCTACCCAGGAAAGTAATAGCT  
 TCTTAAAGTCTTCAAAGGTTGGAAATTAACTTGTCTTAATATATCTTAGGCTTCAA  
 TTATTGGGTGCCTTAAAACCTCAATGAGAATCATGGT

## **FIGURE 24**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732
><subunit 1 of 1, 334 aa, 1 stop
><MW: 36294, pI: 4.98, NX(S/T): 13
MLALAKILLISTLFYSLLSGSHGKENQDINTTQNIAEVFKTMENKPISLESEANLNSDKENI
TTSNLKASHSPPLNLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPPLIHSFVSKVPWNA
PIADEDLLPISAHPNATPALSSENFTWSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVE
PSGWLTTSNDSFTGFTPYQEKTTLQPTLKFTNNSKLFPNTSDPQKENRNTGIVFGAILGAIL
GVSLLTLVGYLLCGKRKTDSFSHRRLYDDRNEPVLRLDNAPEPYDVSFGNSSYYNPTLNSA
MPESEENARDGIPMDDIPPLRTSV
```

**Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 235-262

**N-glycosylation site.**

amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,  
163-167, 218-222, 225-229, 298-302, 307-311

## **FIGURE 25**

AACAGGATCTCCTTTGCAGTCTGCAGCCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGC  
 AGCCCCAAGATTCACT**ATG**TGAAAATCGCCTCAATAACCCCTACCGCCGTGAAAAGGGAGG  
 AGGCAGCGCAAGACGTGGAGGCCCTCCTGAGCCGACGGTCAGAACTCAGATACTGACCGGC  
 AAGGAGCTCCGAGTTGCCACCCAGGAAAAGAGGGCTCCTCTGGGAGATGTATGCTTACTCT  
 CTTAGGCCTTCATTCATCTGGCAGGACTTATTGTTGGAGCCTGCATTACAAGTACT  
 TCATGCCAAGAGCACCATTACCGTGGAGAGATGTGCTTTTGATTCTGAGGATCCTGCA  
 AATTCCCTCGTGGAGGAGAGCCTAACCTCCTGCCTGTGACTGAGGAGGCTGACATTGTGA  
 GGATGACAACATTGCAATCATTGATGTGCCTGTCCCCAGTTCTGTGATAGTGACCCCTGCAG  
 CAATTATTCATGACTTGAAAAGGAATGACTGCTTACCTGGACTTGTGCTGGGGAACTGC  
 TATCTGATGCCCTCAATACTTCTATTGTTATGCCTCCAAAAAACTGGTAGAGCTTTGG  
 CAAACTGGCGAGTGGCAGATATCTGCCTCAAACCTATGTGGTCAGAAGACCTAGTTGCTG  
 TGGAGGAAATTGATGTTAGTAACCTGGCATCTTACCAACTTGCAATAACAGA  
 AAGTCCTCCGCCTCGTCGCAGAGACCTCTGCTGGTTCAACAAACGTGCCATTGATAA  
 ATGCTGGAAGATTAGACACTTCCCCAACGAATTATTGTTGAGACCAAGATCTGTCAAGAG**T**  
**AA**GAGGCAACAGATAGAGTGCCTTGGTAATAAGAAGTCAGAGATTACAATATGACTTTAA  
 CATTAAGGTTATGGGATACTCAAGATATTTACTCATGCATTACTCTATTGCTTATGCTTT  
 AAAAGGAAAAAAAAAAACTACTAACCAACTGCAAGCTTGTCAAATTAGTTAAT  
 TGGCATTGCTTGTGAAACTGAAATTACATGAGTTCACTTTCTTGATTTAG  
 GTTTAGATTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAAATTCCATCC  
 GTGTTTTTTGTTGTTGTTCTTCTTAAAGTAAGCTTTATTGATTTAG  
 GTGGAGCAATTAAAATTGAAATATTAAATTGTTGAACTTTGTGAAATATA  
 TCAGATCTAACATTGTTGGTTCTTGTGTTCTTCAATTGACTTACACTTCTGAAATTAGA  
 ATTACATCTTGCAGTTCTGTTAGGTGCTCTGAATTAAACCTGACTTATATGTGAACAAATT  
 TTCATGAGACAGTCATTTAACTAATGCAGTGATTCTTCTCACTACTATCTGATTGTGG  
 AATGCACAAAATTGTGTAGGTGCTGAATGCTGTAAGGAGTTAGGTGTATGAATTCTACAA  
 CCCTATAATAAAATTACTCTACAAAAA

## **FIGURE 26**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828
<subunit 1 of 1, 263 aa, 1 stop
<MW: 29741, pI: 5.74, NX(S/T): 1
MVKIAFNTPTAVQKEEARQDVALLSRTVRTQILTGKELRVATQEKEGSSGRCMLTLLGLSF
ILAGLIVGGACIYKYFMPKSTIYRGEMCFDSEDPANSLRGEPNFLPVTEEADIREDDNIA
IIDVPVPSFSDPAAIIHDFEKGMTAYLDLLLGNCYLMPNNTSIVMPPKNLVELFGKLASG
RYLPQTYVVREDLVAVEEIRDVSNLGIFYQLCNNRKSFRRLRRDLLLGFNKRAIDKCWKIR
HFPNEFIVETKICQE
```

**Type II transmembrane domain:**

amino acids 53-75

**N-glycosylation site.**

amino acids 166-170

**Casein kinase II phosphorylation site.**

amino acids 35-39, 132-136, 134-138

**N-myristoylation site.**

amino acids 66-72, 103-109

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 63-74

## FIGURE 27

GGAGGAGGGAGGGCGGGCAGGCGCCAGCCCAGAGCAGCCCCGGGACCAGCACGGACTCTCT  
 CTTCCAGCCCAGGTGCCCTTCACTCTCGCTCCATTGGCGGGAGCACCCAGTCCTGTACGCC  
 AAGGAACCTGGTCTGGGGCACC**ATG**TTTCGGCGGCAGCCCCAGCCTCCTCATCCTTCTG  
 TTGCTGCTGCTGGGGTCTGTGCCTGCTACCGACGCCGCTCTGTGCCCTGAAGGCCACGTT  
 CCTGGAGGATGTGGCGGGTAGTGGGGAGGCCAGGGCTCGTCGGCCTCCTCCCCGAGCCTCC  
 CGCCACCCCTGGACCCCGCCCTCAGCCCCACATCGATGGGCCAGCACAACCCCTGGGG  
 GCCCATCACCCCCCACAACTCCTGGATGGGATAGTGGACTTCTTCCGCCAGTACGTGAT  
 GCTGATTGCTGTGGTGGGCTCCCTGGCCTTCTGCTGATGTTATCGTCTGTGCCCGGTCA  
 TCACCCGGCAGAACGAGAACGGCCTCGGCCTATTACCCATCGTCCTTCCCCAAGAAGAAGTAC  
 GTGGACCAGAGTGACCGGGCCGGGGCCCTCGGCCTTCAGTGAGGTCCCCGACAGAGCCCC  
 CGACAGCAGGCCAGGAAGCCCTGGATTCCCTCCGGCAGCTCCAGGCCAGATCTGGCCG  
 CCACCCAGAACCTCAAGTCCCCCACCAAGGGCTGCACTGGCGGTGGGACGGAGCCAGGATG  
 GTGGAGGGCAGGGCGCAGAGGAAGAGGAGAACGGCAGCCAGGAGGGGACCAGGAAGTCCA  
 GGGACATGGGTCCCAGTGGAGACACCAGAGCGCAGGAGGAGCCGTGCTCAGGGTCCTTG  
 AGGGGGCTGTGGTGGCGGTGAGGGCAAGGGAGCTGGAAGGGTCTCTTGTAGCCCAG  
 GAAGCCCAGGGACCAGTGGTCCCCCGAAAGCCCTGTGCTTGCAGCAGTGTCCACCCAG  
 TGT**TAA**CAGTCCTCCGGCTGCCAGCCCTGACTGTGGGCCCTCAAGTGGTCACCTCCCC  
 GTGTATGAAAAGGCCTTCAGCCCTGACTGCTTCTGACACTCCCTCCTGGCCTCCCTGTGG  
 TGCCAATCCCAGCATGTGCTGATTCTACAGCAGGCAGAAATGCTGGTCCCCGGTCCCCCGGA  
 GGAATCTTACCAAGTGCATCATCCTCACCTCAGCAGCCCCAAAGGGCTACATCCTACAGC  
 ACAGCTCCCTGACAAAGTGAGGGAGGGCACGTGTCCTGTGACAGCCAGGATAAAACATCC  
 CCCAAAGTGCTGGATTACAGGCAGGTGAGCCACCGTGCCGGCCAAACTACTTTAAAACA  
 GCTACAGGGTAAAATCCTGCAGCACCCACTCTGGAAAATACTGCTCTTAATTTCTGAAGG  
 TGGCCCCCTGTTCTAGTTGGTCCAGGATTAGGGATGTGGGTATAGGGCATTAAATCCTC  
 TCAAGCGCTCTCCAAGCACCCCCGGCTGGGGTGAGTTCTCATCCGCTACTGCTGCTGG  
 GATCAGGTTGAATGAATGGAACCTTCCTGTCTGGCCTCCAAAGCAGCCTAGAAGCTGAGGG  
 GCTGTGTTGAGGGGACCTCCACCCCTGGGAAGTCCGAGGGGCTGGGAAGGGTTCTGACG  
 CCCAGCCTGGAGCAGGGGGCCCTGGCACCCCTGTTGCTCACACATTGCTGGCAGCCTG  
 TGTCCACAATATCGTCAGTCCTCGACAGGGAGCCTGGCTCCGTGCTTGGAGGCT  
 CTGGCAGGAGGTCTCTCCCCATCCCTCCATCTGGGCTCCCCAACCTCTGCACAGCTCT  
 CCAGGTGCTGAGATATAATGCACCAGCACAATAACCTTATTCCGGCCTGAAAAAAAAGA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

## **FIGURE 28**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852
><subunit 1 of 1, 283 aa, 1 stop
><MW: 29191, pI: 4.52, NX(S/T): 0
MVSAAAPSLLLLLLLGSVPATDARSVPLKATFLEDVAGSGEAEGSSASSPSLPPPWTPAL
SPTSMGPQPTTLGGPSPPTNFLDGIVDFRQYVMLIAVVGSLAFLMFIVCAAVITRQKQKA
SAYYPSSFPKKYVDQSDRAGGPRAFSEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSP
TRAALGGGDGARMVEGRGAEEEKGSQEGDQEVQGHGVPVETPEAQEEPCSGVLEGAVVAGE
GQGELEGSLLLQAQEAQGPVGPPESPCACSSVHPSV
```

**Signal peptide:**

amino acids 1-25

**Transmembrane domain:**

amino acids 94-118

**N-myristoylation site.**

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,  
211-217, 238-244, 242-248

## **FIGURE 29**

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGA  
 GGGAGGACAGGGACTCGGAAGGGAGGAGGACAGAGGAGGGCACAGAGACGCAGAGCAAGGGCG  
 GCAAGGAGGAGACCCCTGGTGGGAGGAAGACACTCTGGAGAGAGAGGGGCTGGCAGAG**ATG**  
 AAGTTCCAGGGGCCCTGGCCTGCCTCCTGCTGGCCCTCTGCCTGGCAGTGGGAGGCTGG  
 CCCCTGCAGAGCGGAGAGGAAAGCACTGGACAAATATTGGGAGGCCCTGGACATGGCC  
 TGGGAGACGCCCTGAGCGAAGGGTGGAAAGGCCATTGGCAAAGAGGCCGGAGGGCAGCT  
 GGCTCTAAAGTCAGTGAGGCCCTGGCCAAGGGACCAGAGAAGCAGTTGGCACTGGAGTCAG  
 GCAGGTTCCAGGCTTGGCGCAGCAGATGCTTGGCAACAGGGCAGGGAAAGCAGGCCATG  
 CTCTGGAAACACTGGCACGAGATTGGCAGACAGGCAGAAGATGTCAATTGACACGGAGCA  
 GATGCTGTCCCGGGCTCCTGGCAGGGGTGCCTGCCACAGTGGTGCCTGGAAACTCTGG  
 AGGCCATGGCATCTTGGCTCTCAAGGTGGCCTGGAGGCCAGGGCAATCCTGGAG  
 GTCTGGGACTCCGTGGTCCACGGATAACCCGGAAACTCAGCAGGCAGCTTGGAAATGAAT  
 CCTCAGGGAGCTCCCTGGGTCAAGGAGGCAATGGAGGCCACCAAACCTTGGACCAACAC  
 TCAGGGAGCTGTGGCCCAGCCTGGCTATGGTCAGTGAGAGGCCAGCAACCAGAACATGAAGGGT  
 GCACGAATCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCAACTCTGGGGAGGCAGCGGC  
 TCACAGTCGGGCAGCAGTGGCAGTGGCAGCAATGGTACAACAACAAATGGCAGCAGCAGTGG  
 TGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAGCAGTGGCGGCAGCAGTGGCGGCAGCAGTGG  
 GTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGGAGTCCTGGGAA  
 TCCAGCACCGGCTCCTCCGGCAACCACGGTGGAGCGGGAGGAAATGGACATAAAC  
 CGGGTGTAAAAGCCAGGAATGAAGCCCGGGAGCAGGGAAATCTGGATTAGGGCTTCA  
 GAGGACAGGGAGTTCCAGCAACATGAGGAATAAGCAAAGAGGGCAATCGCCTCTGG  
 GGCTCTGGAGACAATTATCGGGGCAAGGGTCAGCTGGGCAGTGGAGGAGGTGACGCTGT  
 TGGTGGAGTCAATACTGTGAACCTCTGAGACGTCTCTGGATGTTAACCTTGACACTTCT  
 GGAAGAATTAAATCCAAGCTGGTTCATCAACTGGGATGCCATAAACAGGACCAAGA  
 AGCTCTCGCATCCCG**TGA**CCTCCAGACAAGGAGCCACCAGATTGGATGGAGGCCACACT  
 CCCTCCTAAACACCACCCCTCTCATCACTAACTCAGCCCTGCCCTGAAATAACCTTA  
 GCTGCCCAACAAAAAAAAAAAAAA  
 AAAAAAAAAAAAAAA

**FIGURE 30**

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212
><subunit 1 of 1, 440 aa, 1 stop
><MW: 42208, pI: 6.36, NX(S/T): 1
MKFQGPLACLLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGA
AGSKVSEALGQGTREAVGTGVRQVPFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG
ADAVRGSWQGVPGHSGAWETSGGHGIFGSQGGIQQGQGPGLGTPWVHGYPGNSAGSFGM
NPQGAPWGQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGSGGGSSNSGGGS
GSQSGSSGSGSNGDNNNGSSSGSSSGSSGGSSGGSSGGSSGGSGSRGDGSSESSW
GSSTGSSSGNHGGSGGGNGHPGCEKPGNEARGSGESGIQGFRGQGVSSNMREISKEGNRLI
GGSGDNYRGQGSSWGSGGDAVGGVNTVNSETSPGMNFDTFWKNFKSKLGFINWDAINKDQ
RSSRIP
```

**Signal peptide:**

amino acids 1-21

**N-glycosylation site.**

amino acids 265-269

**Glycosaminoglycan attachment site.**

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

**Casein kinase II phosphorylation site.**

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

**N-myristoylation site.**

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,  
 74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,  
 155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,  
 218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,  
 249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,  
 279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,  
 295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,  
 323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,  
 383-389, 387-393, 389-395, 395-401

**Cell attachment sequence.**

amino acids 301-304

## FIGURE 31

GACCGGGTCCCTCCGGTCTGGATGTGCGGACTCTGCTGCAGCGAGGGCTGCAGGCCGCCGGTGCCTCACCG  
 TGCCCTGGCTGGTGGAGTTCTCTCCTTGCTGACCATGTTGTCAGGAGACTGAGGGAAAG**ATGT**TTCCTGAACAAAGC  
 CTCTCCTGCTGCCCTGCACCGGACCTGGTGTGCGCAGGAGACTGAGGGAAAG**ATGT**TTCCTGAACAAAGC  
 TGCTGCTACTTGCTGCTGGCTGGCTTCCAGATTCCCACAGTCCCTGAGGACTTGTCTTCTGGAAGAGG  
 GTCCCTCATATGCCTTGAGGTGGACACAGTAGCCCCAGAGCATGGCTGGACAATGCGCTGTGGTGGACCAGC  
 AGCTGCTCTACACCTGCTGCCCTACATCGGAGAGCTCCGAAACTGCTCGCTTCGTGGTGTCAAGGAGTAGTG  
 GACGGAGTGGGGCTTCATGAGGAAAATCACCCCCCACCACCTACCAACAGCCTGGGAGGCCAGCCTCCAGACCA  
 GCCAGGGCTGCAGGCACAGCTGCCAGGCCCTTCCACAACCAGCCGCCCTCCTGCCGGGACCGTAGAGT  
 TCGTGGCAGAAAGAATTGGATCAAACATGTGTCAAACATATCAAGGCTACACTGGTGGCAGATCTGGTGCAGCAGG  
 CAGAGTCACTTCTCCAAGAGCAGCTGGTACACAGGGAGAGGAAGGGGGAGACCCAGCCAGCTGGAGAGATCT  
 TGTGTTCCCAGCTGTGCCCTCACGGGGCCAGCATTGGCCCTGGGGGGAGTTCTGTCAGGAAAGAGCCCTG  
 GGGCTGTGCGGGCGCTGCTCCAGAGGAGACCCGGCAGCCGTTCTGAGCAGTGCAGAGAACATTGCTGTGGGGC  
 TTGCAACAGAGAAAGCCTGTGCTGGCTGTCAACATCACAGCACTGATCAGGAGGGAGGTGAAAGCAGCAG  
 TGAGTCGCACACTTCGAGCCAGGGCTGAACCTGCTGCCGGGGAGCGGGAGCTGCTCCGCC**TGAC**  
 GTGCTCTCCTGGCCGTGGGCCACGGGACCCCTGACGAGGGAGTCTCCCAGAGCATCTGGAACAGCTCTAGGC  
 CAGCTGGGCCAGCAGCTGCCGCGCCAGTCCCTGTGCCCACCTGTCAGCAGCAGCATCTGCAAAGTGCCTGTG  
 GAGTTAGCTCCCTCCTCGTTGCAAGATCAAATTCTATCCTAGGGCCCCGGCACAGTACAGGCTGGAGAGAGGG  
 CAGGCTCGAAGGCTCTGCACATGCTGCTTCTGTGAGGAAAGAGACTTCAGGGCCGGTCCGCTGCAGCTG  
 CTGCTGAGCCCAAGAAATGTGGGCTTCTGGCAGACACAAGGCAAGGGAGTGGACTTGTGCTATTCTGCTA  
 CGGGAGCTGGTGGAGAAGGGCTGATGGGACGGATGGAGATAGAGGCTGCCCTGGCAGCCCTCACCAGGCCAG  
 TGGCCAGGGACTTGTGAGAAGAATTAGCAACACTGCTAACTCTGTTCTAGCCGAGCCCCACCTGCCAGAACCC  
 CAGCTAAAGAGCCTGTGAGTTGGTGCAGCCAAACCGGGGACTGTGCTGGCCAGAGCTAGGGCTGAGAACGG  
 CTGCTCTGGGCAATTGACACCAGAACCCCTGGACCCCCGCTCACAGGAGGGCCAAGTGCCTGGCAGACCC  
 TGGTTGGGGTAGCTGGGTCTACAGTCAGACTTCTGCTTAAGGGTGTCACTGCCCTGGCATCCCCACAGCGA  
 ATCCTAGAGGAAGGGAGATTGGCCTGATTGGGATTATGGCAGAAAAGTCCAGAGATGCCAGTCTGGAGTAGAA  
 GAGGTGGTTGTTGTTATCTCTGGATAACTAAATGAAATGAGGTGTGTTGGCTGTCAACACAGAAATTCAAGCCT  
 CATTGCTATCCCAGCATCTCTTAAACACTTGTAGTCTGGAAATTGATCACAGAGGGCAAATGACTCCTGCTTAAC  
 TTATGAAAGAAAGTTAAACATGAATCTGGGAGTCTACATTCTTATCACCAGGAGCTGACTGCCATCTCCTT  
 ATAATGCCAACACAGGCCGGCTGGCTCATGCCGTAACTCCAGCACTTGTGAGAGGCCCTGAGGTGGCG  
 GACTGCCGTGGAGTCAGGAATTCAAGACCAGCTGGCAACATGGAAAACCCCATCTCTACTAAAAA  
 TTATTAGCTGGGATGGTGGTGTGCTGTAATCCCAGCTACTCAGGAGGATGAGGCAGGGAGACCTGCTGAAC  
 CTGGAGGTGGAGGTTGCACTGAGGCCAGGTCGCCACTGCACTCCAGTCTGGTAACAGAGCGAGACTTTCTAG  
 AAAAACGCTAACAAACAGATAAGTAGGACTCAACCAACTGAAACCTGACTTTCCCTGTACCTTCAGCCCTG  
 TGCAGGTAGTAACCTCTTGAGACCTCCCTGACCGAGGACCAAGCACAGGGCATTTAGAGCTTTTAA  
 CTGGTTTCTTAAAAAAGGGCTTTATTAAATCTCCCCACAGATGGCTCTGCAATCTGCCACAGCTC  
 TGGGGCTGCTGTAGGAAAGGCCCTGTTCCCTGAGGCCGGCTGGCTTGTCCATGGTCCGGAGCTG  
 GCCGTGCTGGGCCCTGGCGTGTGCTAGTGTCTTGTGCGGGCACAGAGCTGCCGGCTGGGGGACCCGGG  
 AGCTAAGAGCAGGCTCTGGTGCAGGGGTGGAGGCCTGTCTTAACCGACACCCCTGAGGTGCTCTGAGATGCTG  
 GGTCACCCCTGAGTGGCACGGGGAGCAGCTGTCGGCGGTGCTCCCTCYAGGCCAGTCTGGGAAACTAAGCTC  
 GGGCCCTTCTTGCACAGGAGATGGGGTGGGTGAGGGACTCATGGGAATGGCTGAGGAGCTACGTGT  
 GAAGAGGGGCCGGTTGGCTGCAGGCCCTGGAGGCCCTCTCCTGAGGCTCAGTTCCCTTCCGTCTA  
 ATGAAGAACATGCCGTCTCGGTGTCTCAGGGCTATTAGGACTTGCCCTCAGGAAGTGGCCTGGACGAGCGTCAT  
 GTTATTTACAACACTGTCTGCGACGTGGCTGGCACGTGAGGAGGCCAGACGTGCGCCCTGGGGTGA  
 GGGGGAGGCCAGGGCCACCCAGGCAGGGGGCTCCGCCGCCGCCACCGTCCAGG  
 CCTCACAGGAAGTGGAGTGGCTCCGCACCCAGGCAGGGGGCTCCGCCGCCACCGTCCAGG  
 GGCGGTAGACAAAGTGGAGTGGCTGCGCTGGGCTGCGCAGCAGGTAGCCCTTGATGCA  
 GAGTGCAGGCCAGCGCCTGCGCCT

## **FIGURE 32**

MCFLNKLLLLAVLGWLFQIPTVPEDLFFLEEGPSYAFEVDTVAPEHGLDNAPVVDQQQLLYTC  
CPYIGELRKLLASWVSGSSGRSGGFMRKITPTTTSLGAQPSQTSQLQQAQLAQAFFHNQPP  
SLRRTVEFVAERIGSNCVKHIKATLVALVRQAESLLQEQLVTQGEEGGDPAQLLEILCSQL  
CPHGAQALALGREFCQRKSPGAVRALLPEETPAAVLSSAENIAVGLATEKACAWLSANITAL  
IRREVKAAVSRTLRAQGPEPAARGERRGCSRA

**Signal peptide:**

amino acids 1-18

**N-glycosylation site.**

amino acids 244-248

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 89-93

**Casein kinase II phosphorylation site.**

amino acids 21-25, 167-171, 223-227

**N-myristoylation site.**

amino acids 100-106, 172-178, 207-213

**Microbodies C-terminal targeting signal.**

amino acids 278-282

## **FIGURE 33**

TCCCTTGACAGGTCTGGTGGCTGGTCGGGCTACTGAAGGCTGTCTGATCAGGAAACTG  
AAGACTCTGCTTTGCCACAGCAGTCCCTGCAGCTCCTTGAGGTGTGAACCCACATCCC  
TGCCCCCAGGGCCACCTGCAGGACGCCACCTACCCCTCAGCAGACGCCGGAGAGAA**ATG**  
AGTAGCAACAAAGAGCAGCGGTCAAGCAGTGTGATCCTCTTGCCCTCATCACCATCCT  
CATCCTCTACAGCTCAACAGTCCAATGAGGTCTTCCATTACGGCTCCCTGCAGGGCCGTA  
GCCGCCGACCTGTCAACCTCAAGAAGTGGAGCATCACTGACGGCTATGTCCCCATTCTCGGC  
AACAAAGACACTGCCCTCTGGTGCACCAGTGTGATTGTCAAGCAGCTCCAGCCACCTGCT  
GGCACCCAAGCTGGGCCCTGAGATCGAGCAGGGCTGAGTGTACAATCCGATGAATGATGCAC  
CCACCACTGGCTACTCAGCTGATGTGGCAACAAGACCACTACCGCGTGTGGCCATTCC  
AGTGTGTTCCCGTGTGAGGAGGCCAGGAGTTGTCAACCAGGACCCCTGAAACCGTGT  
CATCTTCTGGGGGCCCGAGCAAGATGCAGAAGCCCCAGGGCAGCCTCGTGCATGATCC  
AGCGAGCGGGCTGGTGTCCCCAACATGGAAGCATATGCCGTCTCTCCGGCCGATGCGG  
CAATTGACGACCTCTCCGGGTGAGACGGCAAGGACAGGGAGAAGTCTCATTGTGGTT  
GAGCACAGGCTGGTTACCATGGTGTGACGCCAGCAGGGCCCTCCAGCGCATGCCCTACCACTAC  
GCATGGTCCCCCCCCAACTACTGCAGCCAGCAGGGCCCTCCAGCGCATGCCCTACCACTAC  
TACGAGCCAAGGGCCGGACGAATGTGTCACCTACATCCAGAATGAGCACAGTCGAAGGG  
CAACCACCACCGCTTCATCACCAGAAAAGGGCTTCTCATCGTGGGCCAGCTGTATGGCA  
TCACCTTCTCCCACCCCTGGACC**TAG**GCCACCCAGCCTGTGGGACCTCAGGAGGGTCAG  
AGGAGAACGCCTCCGCCAGCCGCTAGGCCAGGGACCATCTCTGGCCAATCAAGGCTTG  
CTGGAGTGTCTCCAGCCAATCAGGGCCTTGAGGAGGATGTATCCTCCAGCCAATCAGGGCC  
TGGGAATCTGTTGGGAATCAGGGATTGGGAGTCTATGTGGTTAATCAGGGGTGTCTTC  
TTGTGCAGTCAGGGTCTGCGCACAGTCAATCAGGGTAGAGGGGGTATTCAGTCAATCTG  
AGGCTAAGGACATGTCTTCCATGAGGCCTGGTTAGAGGCCAGGAATGGACCCCCCA  
ATCACTCCCCACTCTGCTGGATAATGGGGCTGTCCAAGGAGCTGGAACTTGGTGT  
CCCCCTCAATTCCAGCACCAAGAGAGATTGTGTGGGGTAGAAGCTGTCTGGAGGCC  
GGCCAGAGAATTGTGGGTTGTGGAGGTTGTGGGGCGGTGGGAGGTCCCAGAGGTGGGA  
GGCTGGCATCCAGGTCTGGCTCTGCCCTGAGACCTGGACAAACCCCTCCCCCTCTGGG  
CACCTTCTGCCACACCAGTTCCAGTGCAGGAGTCTGAGACCCCTTCCACCTCCCTACAA  
GTGCCCTCGGGTCTGCTCTCCCGTCTGGACCCCTCCAGCCACTATCCCTGCTGGAAAGGCT  
CAGCTCTTGGGGGTCTGGGTGACCTCCCCACCTCCTGGAAAACCTTAAAGGTATTTGC  
GCAAACCTTCAGGGTGGGGACTCTGAAGGAAACGGACAAAACCTTAAGCTGTTTCT  
TAGCCCCCTAGCCAGCTGCCATTAGCTGGCTCTTAAAGGGCAGGCCTCTTCTGCCCT  
CTAGCAGGGAGGTTTCAACTGTTGGAGGCGCTTGGGGCTGCCCTTGTCTGGAGTCA  
CTGGGGCTCCGAGGGTCTCCCTCGACCCCTGTGCTCCTGGATGGCTGTGGAGCTGT  
ATCACCTGGGTCTGCTCCCTGGCTCTGTATCAGGCACTTAAAGCTGGCCTCAGTGG  
GGTGTGTTGTCTCCTGCTCTGGAGCCTGGAAGGAAAGGGCTTCAGGAGGAGGCTGTGA  
GGCTGGAGGGACCAGATGGAGGAGGCCAGCAGCTAGCCATTGCACACTGGGTGATGGGTGG  
GGCGGTGACTGCCAGACTGGTTGTAAATGATTGTACAGGAATAAACACACCTACGC  
TCCGGAAAAAAAAAAAAAA

## **FIGURE 34**

MSSNKEQRSAVFVILFALITILYLSSNSANEVFHYGSLRGRSRRPVNLKKWSITDGYVPIL  
GNKTLPSRCHQCVIVSSSSHILGTKLGEIERAECTIRMNDAPTTGYSADVGNKTYRVVAH  
SSVFRVLRRPQEJVNRTPETVFIFWGPPSKMQKPGSLVRVIQRAGLVFPNMEAYAVSPGRM  
RQFDLFRGETGKDREKSHSWLSTGWFTMVIACHELCDHVHVYGMVPPNYCSQRPRLQRMPYH  
YYEPKGDPDECVTYIQNEHSRKGNHHRFITEKRVFSSWAQLYGITFSHPSWT

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 9-31 (type II)

**N-glycosylation site.**

amino acids 64-68, 115-119

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 50-54

**Casein kinase II phosphorylation site.**

amino acids 3-7, 29-33, 53-57, 197-201

**Tyrosine kinase phosphorylation site.**

amino acids 253-262

**N-myristoylation site.**

amino acids 37-43, 114-120, 290-294

## FIGURE 35

GTTTCTCATAGTGGCGTCTTCTAAAGGAAAAACACTAAAATGAGGAACTCAGCGGACCAGGGAGCGACGCAGCTT  
 GAGGGAAAGCATTCCCTAGCTGTGGCGCAGAGGGCGAGGTGAAGCGAGTGGCCGAGGTGTCTGAGGGGCTGG  
 GCCTAAAGGTGAAAGACTTCAGAACAGCTCTGGAACCCATGACCCATGAAGTCTTGTGACATTATACCGT  
 CTGAGGGTAGCAGCTGAAACTAGAAGAAGTGGAGTGTGCCAGGGACGGCAGTATCTCTTGTGACCCCTGGC  
 GGCTATGGGACGTTGGCTTCAGACCTTGATGACACCACTGCTGCGTGGGAGCAGTGAACGGCTGGAGAGGAATG  
 AGGCCTGAGGTACACTGGCTTGCCTCCTCCTAGCCACAGCAGGCTGCTTGACTTAAGCAGGTCAGCTCCAG  
 GTCACCGTCCAGCCTGCGTCCACGGACTGTGATCTGGCTGCGTGGAGACCTCCA  
 AGGATGAATGTAACCTGGCGCTGAATGGAAGAGCTGAATGGCTCGGATGATGCTCTGGGTGCTCCTCATCACC  
 CACGGGACCCCTCGTCATCACTGCCCCAACACACTGTGGGACGGTACCGTGTGGCCGGATGCCTGCG  
 GGGCTGTGGCCAGCGTGGCAGGACTGTGACACTAGCCAATCTCCAGGACTTAAGTTAGATGTGACAGCTG  
 ATTGAAGTGGATGAGGGAAACACAGCAGTCACTGCTGCACCTGCTGAGAGCCACCCCAAAGGCCAGGTCCGG  
 TACAGCGTCAAACAAGAGTGGCTGGAGGCTCAGAGGTAACACCTGATCATGCCCTCAGGGAACCTCCAGATT  
 GTGAATGCCAGGCCAGGAGGACGAGGGCATGTACAAGTGTGAGCCTACAACCCAGTGACCCAGGAAGTGAACACC  
 TCCCGCTCCAGCGACAGGCTACGTGTGCGCCGCTCCACCGCTGAGGTGCCCAGCATCATCTACCCCCCAGAGGCC  
 CAAACCATCATGTCACCAAAGGCCAGACTCTCATCTGAGGTGTGGCCAGTGGAAATCCCACCCCCACGGGTC  
 ACCTGGGCAAGGATGGGTCAGTCACCGGCTAACAAAGACGCCCTCTGTGAGCAACCTCCTCATCGAC  
 ACCACCGCAGGAGGAGACTCACGGCACCTACCGCTGATGCCGACAATGGGTTGGGAGCCGGCAGCGGTC  
 ATCCTCTACAATGTCAGGTGTTGAACCCCCCTGAGGTACCATGGAGCTATCCCAGCTGGTCATCCCCGGGG  
 CAGAGTGCACAGCTTACCTGTGAGGTGCGTGGGAAACCCCCCGCCCTCCGTGCTGTGGCTGAGGAATGCTGTG  
 CTCATCTCCAGGCCAGCGCCTCCGGCTCTCCCGCAGGGCCCTGCGCGTCTGAGCATGGGGCTGAGGAAGGC  
 GTCTACCAAGTGCATGGCGAGAACGAGGTGGGAGCGCCATGCCGTAGTCCAGCTGCCAGCTCCAGGCAAGC  
 ATAACCCCAAGGATGGCAGGATGCTGAGCTGGCTACTGGCACACCTCTGTATCACCTCCAAACTCGGCAAC  
 CCTGAGCAGATGCTGAGGGGCAACCGCGCTCCCGCAGACCCCCAACGTCAGTGGGGCTGCTTCCCCAGGT  
 CCAGGAGGAGAGGGCAGGGGCTCCCGCAGGCTCCCATCATCCTCAGTCGCCCCCGCACCTCCAAGACAGAC  
 TCATATGAACTGGTGTGGCGGCCTCGGATGAGGGCAGTGGCCGGGCGCAATCCTCTACTATGTGGTGAACAC  
 CGCAAGCAGGTACAAATTCTCTGACGATTGGACCATCTGGCATTCCAGCCAACCGACCGCCTGACCC  
 ACCAGACTTGACCCCGGGAGCTTGTATGAAGTGGAGATGGCAGCTTACAACACTGTGCGGGAGAGGGCCAGACAGC  
 ATGGTCACCTTCCGAACTGGACGGCGCCAAACCCGAGATCATGGGCAGCAGACAGATCCAGAGAGAC  
 GACCCCTGGAGGGCAGTCCCGAGACGAGCAGCCAGCACACGCCGCGCTCTCCCCCGAGAAGCTCCGACAGG  
 CCCACCATCTCACGGCCTCCGGAGACCTCAGTGTACGTGACCTGGATTCCCCGGGAAATGGTGGGTCTCCAATC  
 CAGTCCTTCCGTGGAGTACAAGAAGCTAAAGAAGTGGGAGACTGGATTCTGGCCACCAGGCCATCCCCCA  
 TCGCGCTGTCGTGGAGATCACGGCCTAGAGAAAGGCACCTCTACAAGTTGAGTCCGGCTCTGAACATG  
 CTGGGGAGAGCGAGCCCAGCGCCCCCTCTGCCCTACGTGGTGTGGCTACAGCGGTGCGTGTACGAGAGG  
 CCCGTGGCAGGTCTTATATCACCTCACGGATGCGGTCAATGAGACCACCATATGCTCAAGTGGATGTACATC  
 CCAGCAAGTAACAACACCCCAATCCATGGCTTATATCTATTATGACCCACAGACAGTACAATGATA  
 GACTACAAGAAGGATATGGTGAAGGGGAAAGTACTGGCAGCTTACAGGCCACCTCAGGCCACAGCAGAGACCTCCTAC  
 GACATTAAGATGCACTGCTTCATGAAGGAGGGGAGAGCGAGTTCAGCAACAGTGTATGTCAGGACCAAAGCT  
 CGGAAGTCTCTGCCAGCCTGGTCACTGCCACCCCCAACACTCTGGCCCCACACAGCCGCCCTCTGAAACC  
 ATAGAGCGGCCGGTGGGACTGGGCCATGGTGGCTCGCTCCAGCGACCTGCCCTATCTGATTGTCGGGCTGTC  
 CTGGGCTCCATCGTCTCATCGTACCTCATCCCCCTCTGCTGTGGAGGGCTGGCTAAGCAAAACAT  
 ACAACAGACCTGGTTTCCTGAAAGTGCCTCCACCCCTCTGCCGTATAACTATGGTGCCTGGGAGGACTC  
 CCAGGCCACCAGGCCAGTGGACAGCAGCTACCTCAGTGGCATGAGGGCCTGCTGCTAATGGGATCCACATG  
 AATAGGGGCTGCCCTCGGCTGAGTGGGCTACCCGGCATGAAGGCCAGCAGCACTGCCAGGCCAGCTT  
 CAGCAGAGTGAACACAGCAGCCTGAGGAGACCCATCTGGCAATGGATATGACCCCCAAAGTCACCA  
 ACGAGGGTCCAAGTCTAGCCGGACGAGGGCTTTCTTATACACACTGCCGACGACTCCACTCACCAGCTG  
 CTGAGCCCCCATCACGACTGCTGCCAACGCCAGGAGCAGCCTGCTGTGGGCCAGTCAGGGGTGAGGAGGCC  
 CCCACAGTCTGCTGGAAAGCAGTGTGGACCCCTCCATTCACTCAGGGCCCCCATGCTGCTGGCCTTGTG  
 CCAGTGTGAAGAGGTGGACAGTCTGACTCTGCCAAGTGAAGTGGAGGAGACTGGTGTCCCCAGCACCCGTAGGG  
 GCCTACGTAGGGACAGGAACCTGGAATGCAGCTCTCCCGGGGCACTGGTGTGTCTTGTGAAACACCACCT  
 CTCACAAATTAGCAGAAAGCTGATATCCCAGAAAGACTATATATTGTTTTTTTAAAGAAGAAAAAA  
 AGAGACAGAGAAAATTGGTATTATTTCTATTATAGCATATTATATGCACTGTAATAAATGTA  
 TATGTTTATAATTCTGGAGAGACATAAGGAGTCCTACCGTTGAGGTGGAGAGGGAAAATAAGAAGCTGCCA  
 CCTAACAGGAGTCACCCAGGAAAGCACCGCACAGGCTGGCGGGACAGACTCTAACCTGGGCCCTGCA  
 GCAGGCGAGGCTGCAGGAGGCCACAGATAAGCTGGCAAGAGGAAGGATCCCAGGCACATGGTTCATCAC  
 TGAGGGAAACAGCAAGGGGACGGTATCACAGCCTGGAGACACCCACACAGATGGCTGGATCCGGTGTAC  
 ACATTTCCTAAAGATGCCCATGAGAACAGACCAAGAGATGTGACAGCACTATGAGCATTAAAAACCT  
 TCCAGAATCAATAATCCGTGGCAACATATCTGTAAAAACAAACACTGTAACCTCTAAATAATGTTAG  
 TCTCCCTGTAAAA

## **FIGURE 36**

MLRGTMATAWRGMRPEVTLACLLLATAGCFADLNEVPQVTVQPASTVQKPGGTIVLGCVVEPP  
 RMNVTWRLNGKELNGSDDALGVLITHGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTL  
 ANLQDFKLDVQHVIEVDEGNTAVIACHLPESHPKAQVRYSVKQEWLEASRGNYLIMPSGNLQ  
 IVNASQEDEGMYKCAAYNPVTQEVKTSGSSDRLRVRRSTAEEAARIIYPPEAQTIIVTKGQSL  
 ILECVASGI PPPRVTWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVGQPGA  
 AVILYNVQVFEPPEVTMELSQLVIPWGQSAKLTCERGNPPPSVLWLRNAVPLISSQLRLS  
 RRALRVLSMGPEDEGVYQCMAENEVGSAAHVVQLRTSRPSITPRLWQDAELATGTPPVSPSK  
 LGNPEQMLRGQPALPRPPTSVGAPSPKCPGEKGQGAPAEAPIIILSSPRTSKTDSYELVWRPR  
 HEGSGRAPILYYVVKHRKQVTNSSDDWTISGIPANQHRLTLTRLDPGSLYEVEMAAYNCAGE  
 GQTAMVTFRGRRPKPEIMASKEQQIQRDDPGASPQSSQPDHGRLSPPEAPDRPTISTASE  
 TSVYVTWI PRGNGGFPIQSFRVEYKKLKVGDWILATS AIPPSRLSVEITGLEKGTSYKFRV  
 RALNMLGESEPSAPS RPYVVSGYSGRVYERPVAGPYITFTDAVNETTIMLKWMYIPASNNT  
 PIHGFYIYYRPTDSDNDSDYKKDMVEGDKYWH SISHLQPETSYDIKMOCFNEGGEFSNVM  
 ICETKARKSSGQPGRLPPPTLAPPQPLPETIERPVGTGAMVARSSDL PYLIVGVVLGSIVL  
 II VTFIPFCLWRAWSKQKHTTDLGFP RSALPPSCP YTMVPLGGLPGHQASGQPYLSGISGRA  
 CANGIHMNRCCPSAAVGYPGMKPQQHCPGELQQQSDTSSLIRQTHLGNGYDPQSHQITRGPK  
 SSPDEGSFLYTL PDDSTHQLLQPHDCCQRQE QPAAVGQSGVRRAPDSPVLEAVWDPPFHSG  
 PPCC LGLVPVEEV DSDP DSCQVSGGDWCPQHPVGAYVGQEPGMQLSPGPLVRVS FETPPLTI

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 16-30 (type II), 854-879

## **FIGURE 37**

CGGGAGGCTGGGTGTCATGATCCGGACCCATTGTCGGCCTCTGCCCATGCCTGCTCCTC  
 CCAGGCTCCCGCGGCCGACCCCCGCGCAAC**ATG**CAGCCCACGGGCCCGAGGGTTCCCGCG  
 GCTCAGCCGGCGGTATCTGCGCGTCTGCTGCTCCTGCTACTGCTGCTGCTGCTGCGGCAGC  
 CCGTAACCCGCGGGAGACCACGCCGGCGCCCCAGAGCCCTCTCCACGCTGGCTCCCC  
 AGCCTCTTACCAACGCCGGGTGTCAGCGCCCTCACTACCCAGGCCTCACTACGCCAGG  
 CACCCCCAAAACCTGGACCTCGGGTCGCGCGAGGCCCTGATGCGGAGTTCCACTCG  
 TGGACGGCCACAATGACCTGCCAGGTCCTGAGACAGCGTTACAAGAATGTGCTTCAGGAT  
 GTTAACCTGCGAAATTTCAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGCCCTCGT  
 GGGTGCCAGTTCTGGTCAGCCTCCGTCTCATGCCAGTCCCAGGACCAGACTGCCGTGCGCC  
 TCGCCCTGGAGCAGATTGACCTCATTCACCGCATGTGTGCCTCCTACTCTGAACCTGAGCTT  
 GTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAGCTGGCCTGCCTCATGGCGTGNAGGG  
 TGGTCACTCACTGGACAGCAGCCTCTGTGCTGCGCAGTTCTATGTGCTGGGGTGCGCT  
 ACCTGACACTTACCTCACCTGCAGTACACCATGGCAGAGAGTTCCACCAAGTTCAGACAC  
 CACATGTACACCAACGTCAAGCGGATTGACAAGCTTGGTGAGAAAGTAGTAGAGGAGTTGAA  
 CCGCCTGGGCATGATGATAGATTGTCCTATGCATGGACACCTGATAAGAAGGGCCTGG  
 AAGTGTCTCAGGCTCCTGTGATCTTCTCCACTCAGCTGCCAGAGCTGTGTGACAATTG  
 TTGAATGTTCCCGATGATATCCTGCAGCTCTGAAGAACGGTGGCATCGTGTGGACT  
 GTCCATGGGGTGCTGCAGTGCAACCTGCTGCTAACGTGTCCTGTGGCAGATCACTTG  
 ACCACATCAGGGCAGTCATTGGATCTGAGTTCATGGGATTGGTGAAATTATGACGGGACT  
 GGCGGTTCCCTCAGGGCTGGAGGATGTGTCCACATACCCAGTCCTGATAAGAGGAGTTGCT  
 GAGTCGTASCTGGAGCGAGGAAGAGCTCAAGGTGTCCTCGTGGAAACCTGCTGCGGGTCT  
 TCAGACAAGTGGAAAAGGTGAGAGAGGGAGAGCAGGGCGCAGAGCCCCGTGGAGGCTGAGTT  
 CCATATGGCAACTGAGCACATCCTGCCACTCCCACCTCGTGCCTCAGAATGGACACCAAGGC  
 TACTCATCTGGAGGTGACCAAGCAGCCAACCAATGGGCTCCCTGGAGGTCCCTCAAATGCCT  
 CCCCATACCTTGTCCAGGCCTTGTGGCTGCCACCATCCAACCTCACCCAGTGGCTC  
 TG**TGA**CACAGTCGGTCCCCGAGAGGTCACTGTGGCAAAGCCTCACAAAGCCCCCTCCT  
 AGTTCAATTACAAGCATATGCTGAGAATAACATGTTACACATGGAAAA

**FIGURE 38**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817
><subunit 1 of 1, 487 aa, 1 stop, 2 unknown
><MW: 53569.32, pI: 7.68, NX(S/T): 5
MQPTGREGSRALSRRYLRRLLLLLRLQPVTRAETTPGAPRALSTLGSPSLFTTPGVPS
ALTPGLTPGTPKTLDLRGRAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLRNFSHGQ
TSLDRLRDGLVGAQFWASVSCQSQDQTAVRLALEQIDLIHRMCASYSELELVSAEGLNSS
QKLA CLIGVXGGHSLDSSLVLSFYVLGVRYLTLCSTPWAESSTKFRHHMYTNVSGLT
SFGEKVVEELNRIGMMIDL SYASDTLIRR VLEVSQAPVIFSHSAARAVCDNLLNPDDILQL
LKNGGIVMVTL SMGV LQCNLLANVSTVADHFDHIRAVIGSEFIGIGGNYDGTGRFPQGLEDV
STYPV LIEELLSRXWSEEELQGVLRGNLLRVFRQVEK VREESRAQSPVEAEFPYQQLSTSCH
SHLVPQNGHQATHLEVTKQPTNRVPWRSSNASPYLVPGLVAAATIPTFTQWL C
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-36

**Transmembrane domain:**

amino acids 313-331

**N-glycosylation sites.**

amino acids 119-122, 184-187, 243-246 and 333-336

**N-myristoylation sites.**

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 136-146

## **FIGURE 39**

TGCTAGGCTCTGTCCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGA  
 TCCCTCTATGACTGCAATGTGAGGTGTCGGCTTGCTGGCCAGCAAGCCTGATAAGC**ATG**  
 AAGCTCTTATCTTGGTGGCTGTGGTGGGTGTTGCTGGTGCCAGCTGAAGCCAACAA  
 GAGTTCTGAAGATATCCGGTGCACCGAGAATGCATCTGTCCACCTTATAGAAACATCAGTGGGCACA  
 TTTACAACCAGAATGTATCCCAGAAGGACTGCAACTGCCTGCACGTGGTGGAGCCCAGGCCA  
 GTGCCTGGCCATGACGTGGAGGCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAG  
 CACCACCACCATCAAGGTACATTGTCATCTACCTGTCCGTGGTGGGTGCCCTGTTGCTCT  
 ACATGGCCTTCCTGATGCTGGTGGACCCCTGATCCGAAAGCCGGATGCATACACTGAGCAA  
 CTGCACAATGAGGAGGAGAATGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCATCCCTCGG  
 GGGACCCCCAGCAAACACAGTCCTGGAGCGTGTGGAAGGTGCCAGCAGCGGTGGAAGCTGC  
 AGGTGCAGGAGCAGCGGAAGACAGTCAGTGGCACAAGATGCTCAGC**TAG**ATGGGCTGG  
 TGTGGTTGGGTCAAGGCCAACACCATGGCTGCCAGCTCCAGGCTGGACAAAGCAGGGGG  
 CTACTTCTCCCTCCCTCGGTTCCAGTCTTCCCTTAAAAGCCTGTGGCATTTCCTCCTT  
 CTCCCTAACCTTAGAAATGTTGACTTGGCTATTTGATTAGGAAAGAGGGATGTGGTCTCT  
 GATCTCTGTTGTCCTGGGTCTTGGGTTGAAGGGAGGGGAAGGCAGGCCAGAAGGGA  
 ATGGAGACATTGAGGCCCTCAGGAGTGGATGCGATCTGTCTCCTGGCTCCACTCTG  
 CCGCCTTCCAGCTCTGAGTCTGGGAATGTTGTTACCTTGGAAAGATAAAAGCTGGGTCTTCA  
 GGAACTCAGTGTCTGGGAGGAAAGCATGGCCAGCATTAGCATGTGTTCTTCTGCAGTG  
 GTTCTTATCACCAACCTCCCTCCCAGCCCCGGCGCCTCAGCCCCAGCCCCAGCTCCAGCCCTG  
 AGGACAGCTCTGATGGGAGAGCTGGGCCCCCTGAGCCCAGTGGCTTCAGGGTGCAGTG  
 AGCTGGTGGTCGCTGTCCTGCACTTCTCGCACTGGGCATGGAGTGCCAGTCATACT  
 CTGCTGCCGGTCCCTCACCTGCACTTGAGGGGTCTGGCAGTCCCTCTCCCCAGTGTG  
 CACAGTCAGTGGCCAGACGGTCGGTTGAAACATGAGACTCGAGGCTGAGCGTGGATCTGAA  
 CACCACAGCCCCTGTACTGGGTTGCCTCTGTCCCTGAACCTCGTTGTAACAGTGCATGGA  
 GAGAAAATTTGTCCTTGTCTTAGAGTTGTTGAAATCAAGGAAGCCATCATTAAATTG  
 TTTTATTCCTCTCA

## **FIGURE 40**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278
<subunit 1 of 1, 183 aa, 1 stop
<MW: 20574, pI: 6.60, NX(S/T): 3
MKLLSLVAVVGCLLVPPAEANKSSEDIRCKCICPPYRNISGHIYNQNVSQKDCNCLHVVEPM
PVPGHDVAYCLLCECRYEERSTTIKVIIVIYLSVVGALLLYMAFLMLVDPLIRKPDAYTE
QLHNEEENEDARSMAAAASLGGPRANTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS
```

**Important features:**

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 90-112

**N-glycosylation sites.**

amino acids 21-24, 38-41 and 47-50

## FIGURE 41

AGCGGGTCTCGCTGGGTCCGCTAATTCTGCTCTGAGGCCTGAGACTGAGTCATAGGGTCTGGGTCCCCGA  
 ACCAGGAAGGGTGAGGGAACACAATCTGCAAGCCCCCGCACCAAGTGAGGGGCCGTGTTGGGTCCCTCCC  
 TCCCCTTGCATTCCCACCCCTCGGGCTTGCCTCTCCTGGGGACCCCTCGCCGGAGA**TG**GCCCGCTGATG  
 CGGAGCAAGGATTCGTCCTGCCTGCCTACTGGCCGGTGTGATGGTGGAGAGCTCACAGATCGGAGT  
 TCGCAGGGCAAACCTCAACTCCATCAAGTCCTCTGGGGGGAGACGCCTGGTCAAGGCCCAATCGATCTGCG  
 GGCATGTACCAAGGACTGGCATTGGCGAGTAAGAAGGGCAAAACCTGGGCAGGCCTACCCCTGAGCAGT  
 GATAAGGAGTGTGAAGTGGGAGGTATTGCCACAGTCCCCACCAAGGATCATGGCCTGCATGGTGTGCGGAGA  
 AAAAGAAGCGCTGCCACCGAGATGGCATGTGCTGCCAGTACCCGCTGCAATAATGGCATCTGTATCCAGTT  
 ACTGAAAGCATCTTAACCCCTCACATCCCAGCTGGATGGTACTCGGCACAGAGATCGAAACCACGGTCATTAC  
 TCAAACCATGACTGGGATGGCAGAATCTAGGAAGACACACACTAAGATGTACATATAAAGGCATGAAGGA  
 GACCCCTGCCTACGATCATCAGACTGCATTGAAGGGTTTGCTGTGCTGTCATTCTGGACAAAATCTGCAA  
 CCAGTGCTCCATCAGGGGAAAGTCTGTACCAAACAACGCAAGAAGGGTCTCATGGCTGAAATTTCAGCGT  
 TGCGACTGTGCGAAGGGCCTGCTTGCAAAGTATGAAAGATGCCACCTACTCCTCAAAGCCAGACTCCATGTG  
 TGTCAGAAAATT**TG**ATCACCATTGAGGAACATCATCAATTGCAAGACTGTGAAGTTGTATTTAATGCATTATAG  
 CATGGTGAAAATAAGGTTCAGATGCAGAAGAATGGCTAAAATAAGAAACGTGATAAGAATATAGATGATCACAA  
 AAAGGGAGAAAGAAAATGAACTGAATAGATTAGAATGGGTGACAAATGCAAGTCAGTGCAAGCCAGTGT  
 CAACITGTCTATGTAATAATGTACACATTGTTGAAAATGCTATTATTAAGAGAACAGCACAGTGGAAATT  
 ACTGATGAGTAGCATGTGACTTTCAAGAGTTAGGTTGCTGGAGGGAGGGTTCTCAGATTGCTGATTG  
 TTATACAAATAACCTACATGCCAGATTCTATCAACGTTAGAGTTAACAAAATACTCCTAGAATAACTGTTA  
 TACAATAGGTTCTAAAATAATGCTAAACAAGAAATGAAAACATGGAGCATGTTAATTACACAGAAAAT  
 TACCTTTGATTGTAACACTACTCTGCTGTCATCAAGAGTCTGGTAGATAAGAAAAAAATCAGTCATAT  
 TTCCAATAATGCAAATAATGGCAGTTGTTAGGAAGGCCCTTAGGAAGACAAATAACAAACACAG  
 CCACAAATACTTTTCTCAAATAATGTTACCTGTAATTAAAGAAACTGATACAGACAAAACAGTTCC  
 TTCAGATTCTACGGAATGACAGTATATCTCTTCTATCTGATTCTGCTCTGAATGCATTATATTTC  
 AACTATACCCATAAATTGACTAGTAAATACTACACAGAGCAGAAATTTCACAGATGGCAAAAATTTAAA  
 GATGTCAAATATATGTTGAAAAGAGCTAACAGAGAGATCATTATTCTAAAGATTGCCATAACCTATATT  
 GATAGAATTAGATTGGTAATAACATGTATTACATACACTCTGTTAGAATAGAGACTTAAGCTGGATCTGACTG  
 CACTGGAGTAAGCAAGAAAATTGGGAAACTTTCTGTTGTCAGGTTTGGCAACACATAGATCATATGCTG  
 AGGCACAAGTGGCTGTCATCTTGAAACCAGGGGATGCACAGTCTAAATGAATATCTGCATGGATTGCTAT  
 CATAATATTACTATGCAGATGAATTGCACTGAGGTCTGTGCTCCGTACTATCCTCAAATTATTTATTTATAG  
 TGCTGAGATCCTCAAATAATCTCAATTTCAGGAGGTTCAAAAATGTAACCTGCAAGTAGACAGAGTAG  
 TTTCTGTTGCCCTCTATAAGCTCTGACTAGCCAATGGCATCATCCAATTCTCCCAAACCTCTGCAGCATCTG  
 CTTTATTGCCAAAGGGCTAGTTCTGTTCTGCAGCCATTGCGGTTAAAAATATAAGTAGGATAACTGTAAA  
 ACCTGCATATTGCTAATCTATAGACACCACAGTTCTAAATTCTTGAACCAACTTACTACTTTTTAAACTT  
 AACCTCAGTTCTAAATACTTTGTCGGAGCACAAAACAATAAAAGGTTATCTTATAGTCGTGACTTTAAACTTTG  
 TAGACCACAATCACTTTTAGTTCTTTACTTAAATCCCATCTGCAGTCTCAAATTAAAGTTCTCCAGTAG  
 AGATTGAGTTGAGCCTGTTATCTATTAAAATTCACACTCCCACATATTTACTAAGATGATTAAGACTTA  
 CATTCTGCACAGGTCTGCAAAAACAAAATATAAAACTAGTCCATCCAAGAACCAAGTTGTATAACAGGT  
 TGCTATAAGCTGAAATGAAAATGGAACATTCACAAACATTCCCTATATAACAATTATTATTTACAAAT  
 TTGGTTCTGCAATATTCTTCTTATGTCACCCCTTTAAAATTATTGAAAGTAATTATTTACAGGAAATG  
 TTAATGAGATGTATTCTTCTTATAGAGATATTCTTACAGAAAGCTTGTAGCAGAATATATTGCAGCTATTGAC  
 TTTGTAATTAGGAAAATGTATAAAAGATAAAACTTAAATTCTCCCTAAACACTGAAAAA  
 AAAAAAAAAAAAAAAA

## **FIGURE 42**

MAALMRSKDSSCCLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLA  
FGGSKKGKNLGQAYPCSSDKECEVGRYCHSPHQGSSACMVCRKKRCHRDGMCCPSTRCNN  
GICIPVTEILTYPHI PALDGTRHRDRNHHYSNHDLGWQNLGRPHTKMSHIKGHEGDPCRLS  
SDCIEGFCCARHFWTKICKPVLHQGEVCTKQRKKGSHGLEIFQRCDCAKGLSCKWKDATYS  
SKARLHVCQKI

**Signal peptide:**

amino acids 1-25

## **FIGURE 43**

TCTCAATCTGCTGACCTCGT GATCCGCCTGACCTTGT AATCCACCTACCTGGCCTCCAAA  
 GTGTTGGGATTACAGGC GTGAGCCACCGCGCCGGCAACATCACGTTTTAAAAATTGATT  
 TCTTCAAATT CATGGCAAATATTC CCCCCTTAACCTCTTATGTCAGAATGAGGAAGGA  
 TAGCTGCATTATTTAGTCAGTTTCATTGCATAGTAATATTCATGTAGTATTTCTAAG  
 TTATATTTAGTAATT CATATGTTAGATTAGGTTAACATACTTGAGAAACTTG  
**ATGT** GTTTAAAGCCTGGGCAGAAATTCTGTATTGTTGAGGATTGTTCTTTATCCCCCT  
 TTTAAAGTCATCCGTCCTGGCTCAGGATTGGAGAGCTGCACCACCAAAATGGCAAACA  
 TCACCAAGCTCCCAGATTTGGACCAGTTGAAAGCTCCGAGTTGGCCAGTTACCACCA  
 CCAAGTACACAGCAGAATAGTACAAGTCACCCCTACAACACTACTACTTCTGGGACCTCAAGCC  
 CCCAACATCCCAGTCCTCAGTCCTCAGTCATCTGACTCAAATCTAACCTGAGCCATCCC  
 CAGTTCTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCAGTCACTGTTCTCCT  
 CCTGGTTGGAGTCCTTCCTCCCAGGCAAACCTCGAGAATCAACACCTGGAGACAGTCC  
 CTCCACTGTGAACAAGCTTTGCAGCTCCAGCAGCACCATTGAAAATATCTCTGTGCTG  
 TCCACCAGCCACAGCCAAACACATCAAACCTGCTAAGCGCGGATACCCCCAGCTCTAAG  
 ATCCCCAGCTCTGCAGTGGAAATGCCTGGTCAGCAGATGTCACAGGATTAAATGTGCAGTT  
 TGGGGCTCTGGAATTGGGT CAGAACCTTCTCTCTGAATTGGATCAGCTCCAAGCAGTG  
 AAAATAGTAATCAGATTCCCCTCAGCTGTATTGAGCTTTAAGTGAGCCCTTGAATACA  
 TCTTATCAATGACCAGTGCAGTACAGAACTCCACATATACAACCTCCGT CATTACCTCCTG  
 CAGTCTGACAAGCTCATCACTGAATTCTGCTAGTCCAGTAGCAATGTCTCCTTATGACC  
 AGAGTTCTGTGCATAACAGGATCCCACACAAAGCCCTGTGAGTCATCAGAGTCAGCTCCA  
 GGAACCACATGAATGGACATGGGGTGGTCAGTCAGCAGACACTAGACAGTAAGTATAG  
 CAGCAAGCTACTCTGTCACTGGCTGGGCCAACAAACAGAGGAAGAGGAGTAGCTACGTGA  
 TGTGGAAAACACCAGTTGGTCAATGGCTCATTCTGTTAAAGCAGCCCTTTGCTTTTGT  
 TTTGGACCAGGTGTGGCTGTGGTATTAGAAATGTCTTAACCACAGCAAGAAGGGAGGT  
 GGTGGTCTCATATTCTCTGCCCTAATCAGACTGCACCACAAGTGCAGCAGTACAGTATGCAT  
 TTTAAAGATGCTTGGCCAGGCAGGGTGGCTGATGCCATAATCCAGTGCTTGGGGGCC  
 AAGGCAGGCAGATTGCCAAGCTCAGGAGTTGAGACCACCCCTGGCAACATGGTAAACTC  
 TGTCTACTAAAATACGAAAAACTAGCCGGGTGGTGGCGCGCGTGCCTGTAATCCCAG  
 CTACTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGCTACAAAGTGAGACTCC  
 GTCTGAAAAGA

## **FIGURE 44**

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTT  
PSTQQNSTSHPTTTSWDLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAVTVPP  
PGLESFPSQAKLRESTPGDSPSTVNKLQLPSTTIENISVSVHQQPQPKHIKLAKRRIPPASK  
IPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAPSSSENSNQIPISILYSKSLSEPLNT  
SLSMTSAVQNSTYTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPYQSPVSSSESAP  
GTIMNGHGGGRSQQTLDKYSSKLLLWLVPDKQRKRIAHVMWKTPVGQWLIR

**Signal peptide:**

amino acids 1-24

## **FIGURE 45**

GCCGAGTGGGACAAAGCCTGGGCTGGCGGGGCC **ATG** GCGCTGCCATCCGAATCCTGCT  
 TTGGAAACTGTGCTCTGCAGAGCTCTGCTGTTCTCCTGCACTCAGCGGTGGAGGAGACGG  
 ACGCGGGCTGTACACCTGCAACCTGCACCACACTACTGCCACCTTACGAGAGCCTGGCC  
 GTCCGCCTGGAGGTACCGACGGCCCCCGGCCACCCCCGCTACTGGGACGGCGAGAAGGA  
 GGTGCTGGCGGTGGCGCGCGCACCCCGCGCTTGACCTGCGTAACCGCAGGGCACGTGT  
 GGACCGACCGCACGTGGAGGAGGCTAACAGGTGGTGCACGGGACCGGCAGCCGCCGGG  
 GTCCCGCACGACCGCGCGACCGCCTGCTGGACCTTACCGTCGGCGAGCGCCGCCCTA  
 CGGGCCCTTTCTGCGCACCGCGTGGCTGTGGCGCGATGCCCTTGAGCGCGGTGACT  
 TCTCACTGCGTATCGAGCCGCTGGAGGTGCGCCACGAGGGCACCTACTCCTGCCACCTGCAC  
 CACCAATTACTGTGGCCTGCACGAACGCCGCTTCCACCTGACGGTCGCCAACCCCACGC  
 GGAGCCGCCCGGGCTCTCCGGGCAACGGCTCCAGGCCACAGCGGCCAGGGCAGGCCAG  
 ACCCCACACTGGCGCGGCCACAACGTATCAATGTATCGTCCCCGAGAGCCGAGCCCAC  
 TTCTTCCAGCAGCTGGCTACGTGCTGGCACGCTGCTGCTTACCTGCTACTGGTCAC  
 TGTCCTCCTGGCGCCCGCAGCGCCGGAGGCTACGAATACTCGGACAGAAGTCGGAA  
 AGTCAAAGGGGAAGGATGTTAACTTGGCGAGTTGCGCTGTGGCTGCAGGGACCAAGATGTT  
 TACAGGAGTGAGGACATCCAGCTAGATTACAAAAAACATCCTGAAGGAGAGGGCGGAGCT  
 GGCCCACAGCCCCCTGCCTGCCAAGTACATCGACCTAGACAAAGGGTCCGGAAAGGAGAACT  
 GCAAAT**AG**GGAGGCCCTGGCTCTGGCTGGGCTGGCTGGGAGCAGCTGCACCTCTCTGTCTGTGCTC  
 CTCGGGGCATCTCTGATGCTCCGGGCTCACCCCCCTCCAGCGGCTGGTCCCGCTTCC  
 GGAATTGGCCTGGCGTATGCAGAGGCCGCTCCACACCCCTCCCCAGGGCTTGGTGGC  
 AGCATAGCCCCACCCCTGCGGCTTGCTCACGGGTGCCCTGCCACCCCTGGCACAAACC  
 AAAATCCCACGTGATGCCCATCATGCCCTCAGACCCCTCTGGCTCTGCCGCTGGGGCCTG  
 AACACATTCTGGAGGACACTCCCATCAGAACCTGGCAGCCCCAAACTGGGTCAACCTCA  
 GGGCAGGAGTCCCACCTCCAGGGCTTGCTCGTCCGGGCTGGAGATGTTCTGGAGGA  
 GGACACTCCCACAGAACATTGGCAGCCTGAAGTTGGGTCAAGCTGCCAGGAGTCCCAC  
 CCTCCTGGGTGCTGCCTGCCACCAAGAGCTCCCCACCTGTACCAACCATGTGGACTCCAG  
 GCACCATCTGTTCTCCCCAGGGACCTGCTGACTGAATGCCAGCCCTGCTCCTCTGTGTTG  
 CTTGGGCCACCTGGGCTGCACCCCTGCCCTTCTGCCCATCCCTACCTAGCCTTG  
 CTCTCAGCCACCTTGATAGTCACTGGCTCCCTGTGACTTCTGACCCCTGACACCCCTCC  
 GGACTCTGCCCTGGGCTGGAGTCTAGGGCTGGGCTACATTGGCTTCTGACTGGCTGAGGA  
 CAGGGGAGGGAGTGAAGTTGGTTGGGTGCCACTCTCAGCACCCACATTT  
 GCATCTGCTGGTGGACCTGCCACCATCACAATAAGTCCCCATCTGATTTAAAAAAA  
 AAAAA

## **FIGURE 46**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60618
<subunit 1 of 1, 341 aa, 1 stop
<MW: 38070, pI: 6.88, NX(S/T): 1
MALPSRILLWKLVLLQSSAVLLHSAVEETDAGLYTCNLHHHYCHLYESLAVRLEVTDGPPAT
PAYWDGEKEVLA VARGAPALLTCVNRGHVWTDRHVEEAQQVVHWDRQPPGVPHDRADRLLDL
YASGERRAYGPLFLRDRVAVGADA FERGDFSLRIE PLEVADEGTYSCHLHHHYCGLHERRVF
HLTVAE PHA EPPP RGS PGNG S SHSGAPGP DPTI LARGHN VINV PESRAH FFQQLGYV LATL
LLFILLLVTVLLAARRRRGGYEYSDQKSGKSKGDVNLA EFAVAAGDQMLYRSEDIQLDYKN
NILKERAELAHSPLPAKYIDL DKGFRKENCK
```

**Important features:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 237-262

**N-glycosylation site.**

amino acids 205-208

**Cell attachment sequence.**

amino acids 151-154

**Coproporphyrinogen III oxidase proteins.**

amino acids 115-140

## **FIGURE 47**

CGCCGGAGGCAGCGCGGCGTGGCGCAGCGGCAC **ATGCCGTTGTCAGAGGACGACTTT**  
 CAGCACAGTCAAACCTCACGGAACCACAAGCAGCAGTCTCCGAGCTGACCAGGAGGC  
 ACTGCTTGAGAAGCTGCTGGACCGCCCCCTGGCCTGCAGAGGCCGAGGACCGCTTCT  
 GTGGCACATACATCATCTTCTCAGCCTGGCATTGGCAGTCACTGCCATGGAACCTCTT  
 ATCACTGCCAAGGAGTACTGGATGTTCAAACCTCGCAACTCCTCCAGCCCAGCCACCGGGGA  
 GGACCCCTGAGGGCTCAGACATCCTGAACACTTGTAGAGCTACCTTGCCTTGCCTCCACCG  
 TGCCCTCATGCTGTGCCTGGCCAACCTCCTGCTGTCAACAGGGTTGCAGTCACATC  
 CGTGTCCCTGGCCTCACTGACGGTCATCCTGGCCATCTTCATGGTGATAACTGCACTGGTGAA  
 GGTGGACACTTCCTCTGGACCCGTGGTTTTTGCGGTCACCATTGTCTGCATGGTGATCC  
 TCAGCGGTGCCCTCACTGTCTCAGCAGCAGCATCACGGCATGACCGGCTCCTTCCTATG  
 AGGAACCTCCAAGCAGCAGTGAATATCAGGAGGGACCATGGGCGGGACGGTCAGCGCCGTGGCCTC  
 ATTGGTGGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTTCCTGACGG  
 CCACCATCTCCTCGTCTGCATGGACTCTACCTGCTGCTGTCAGGCTGGAGTATGCC  
 AGGTACTACATGAGGCCTGTTCTGGCCCATGTGTTCTGGTAAGAGGGAGCTCCCCA  
 GGACTCCCTCAGTGCCTTCGGTGGCCTCCAGATTGATTCCCACACACCCCCCTCTCC  
 GCCCCATCCTGAAGAAGACGGCAGCCTGGCTCTGTGTCACCTACGTCTTCATCACC  
 AGCCTCATCACCCGCCGTGCACCAACATCGAGTCCTCAACAAGGGCTCGGGCTCACT  
 GTGGACCACCAAGTTTCATCCCCCTCACTACCTTCCTGTACAACATTGCTGACCTAT  
 GTGGCCGGCAGCTCACGCCTGGATCCAGGTGCCAGGGCCAACAGCAAGGCGCTCCAGGG  
 TTCGTGCTCTCGGACCTGCTCATCCCCCTTCGTGCTGTAACTACCAGCCCCCGGT  
 CCACCTGAAGACTGTGGTCTTCAGTCCGATGTGATCCCCGACTCCTCAGCTCCGCTGG  
 GGCTCAGCAACGGCTACCTCAGCACCCCTGGCCCTCTACGGGCTAAGATTGTGCCAGG  
 GAGCTGGCTGAGGCCACGGGAGTGGTGATGTCCTTTATGTGTGCTGGCTAACACTGGG  
 CTCAGCCTGCTCACCCCTGGTCACCTCATC **TAGAAGGGAGGACACAAGGACATTGGTG**  
 CTTCAGAGCCTTGAAGATGAGAAGAGAGTGCAGGAGGGCTGGGGCCATGGAGGAAAGGCC  
 TAAAGTTCACTGGGGACAGAGAGCAGACACTCGGGCCTCATCCCTCCAAAGATGCCA  
 GTGAGCCACGTCCATGCCATTCCGTGCAAGGCAGATATTCCAGTCATATTAAACAGAACACT  
 CCTGAGACAGTTGAAGAAGAAATAGCACAAATCAGGGTACTCCCTCACAGCTGATGGTTA  
 ACATTCCACCTTCTTAGCCCTCAAAGATGCTGCCAGTGTGCTGCCCTAGAGTTATTACA  
 AAGCCAGTGCCAAAACCCAGCCATGGCTTTGCAACCTCCAGCTCGCCTCATCCAGCT  
 GACAGCGAGATGCAAGCAAATGCTCAGCTCTCCATTACCCCTGAAGGGTCTCCCTGGAATGGA  
 AGTCCCCTGGCATGGTCAGTCCTCAGGCCAAGACTCAAGTGTGCACAGACCCCTGTGTTCT  
 GCAGGGTGAACAACTGCCACTAACCAAGAGACTGGAAAACCCAGAAAGATGGGCTTCCATGAAT  
 GCTCATTCCAGAGGGACCAGAGGGCTCCCTGTGCAAGGGATCAAGCATGTCTGGCCTGGG  
 TTTCAAAAAAAAGAGGGATCCTCATGACCTGGTGGTCTATGGCCTGGGTCAAGATGAGGGTC  
 TTTCAGTGTCCCTGTTACAACATGTCAAAGCCATTGGTTCAAGGGCGTAATAAAACTTGC  
 GTATTCAAAA

## **FIGURE 48**

MAVVSEDDFQHSSNSTYGTTSRADQEALLEKLLDRPPPGLQRPEDRFCGTYIIFSLGI  
GSLLPWNFFITAKEWMFKLRNSSLATGEDPEGSDILNYFESYLAVASTVPSMLCLVANFL  
LVNRVAVHIRVLASLTVILAIFMVITALVKVDTSSWTRGFFAVTIVCMVILSGASTVFSSSI  
YGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSDVRNSALAFFLTATIFLVLCMGLY  
LLLSRLEYARYYMRPVLAHVFSGEEELPQDSLSAPSVASRFIDSHTPPLRPILKKTASLG  
CVTYVFFITSЛИYPAVCTNIESLNKGSGSLWTTKFFIPLTFLLYNFADLCGRQLTAWIQVP  
GPNSKALPGFVLLRTCLIPLFVLCNYQPRVHLKTVVFQSDVYPALLSLLGLSNGYLSTLAL  
LYGPKIVPRELAEATGVVMSFYVCLGLTLGSACSTLLVHLI

**Transmembrane domain:**

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252,  
305-330, 448-472

## FIGURE 49

GACAGTGGAGGGCAGTGGAGAGGACCGCGCTGTCCTGCTGTCACCAAGAGCTGGAGACACCA  
 TCTCCCACCGAGAGTC**ATG**CCCCATTGGCCCTGCACCTCCTCGCCTCGTCCCCATCCTCC  
 TCAGCCTGGTGGCCTCCCAGGACTGGAAGGCTGAACGCAGCCAAGACCCCTCGAGAAATGC  
 ATGCAGGATCCTGACTATGAGCAGCTGCTCAAGGTGGTGACCTGGGGCTCAATCGGACCCT  
 GAAGCCCCAGAGGGTGATTGTGGTTGGCGCTGGTGTGGCCGGCTGGTGGCCGCCAAGGTGC  
 TCAGCGATGCTGGACACAAGGTACCATCCTGGAGGCAGATAACAGGATGGGGGCCGATC  
 TTCACCTACCGGGACCAGAACACGGGCTGGATTGGGAGCTGGGAGGCCATGCGCATGCCAG  
 CTCTCACAGGATCCTCCACAAGCTCTGCCAGGGCTGGGCTCAACCTGACCAAGTCACCC  
 AGTACGACAAGAACACGTGGACGGAGGTGCACGAAGTGAAGCTGCGCAACTATGTGGTGGAG  
 AAGGTGCCCGAGAAGCTGGCTACGCCCTGCGTCCCCAGGAAAAGGGCCACTGCCCGAAGA  
 CATCTACCAAGATGGCTCTCAACCAGGCCCTCAAAGACCTCAAGGCACTGGCTGCAGAAAGG  
 CGATGAAGAAGTTGAAAGGCACACGCTCTTGAATATCTCTGGGGAGGGAACCTGAGC  
 CGGCCGGCCGTGCAGCTCTGGAGACGTGATGTCCGAGGATGGCTTCTTATCTCAGCTT  
 CGCCGAGGCCCTCCGGGCCACAGCTGCCCTGCGCAGACTCCAGTACAGCCGCATCGTGG  
 GTGGCTGGACCTGCTGCCCGCGCTGCTGAGCTCGCTGTCCGGCTTGTGCTGTTGAAC  
 GCGCCCGTGGTGGCGATGACCCAGGGACCGCACGATGTGCACGTGCAGATCGAGACCTCTCC  
 CCCGGCGCGGAATCTGAAGGTGCTGAAGGCCGACGTGGTGTGCTGACGGCGAGCGGGACCGG  
 CGGTGAAGCGCATCACCTCTGCCGCCGCTGCCCGCACATGCAGGAGGCGCTGCCGGAGG  
 CTGCACTACGTGCCGCCACCAAGGTGTTCTAACGCTCCGCAGGCCCTCTGGCGCGAGGA  
 GCACATTGAAGGCCGCACTCAAACACCGATGCCCGTCGCGCATGATTTCTACCGCCGC  
 CGCGCAGGGCGCGCTGCTGGCTCGTACACGTGGTGGACGCCGGCAGCGTTCGCC  
 GGCTTGAGCCGGAAAGAGGCCTGGCGCTCGACGACGTGGCGGCATTGCACGGGCC  
 TGCGTGCAGCTCTGGACGGCACCGCGCTGCTAACGCTTGGCGAGGACAGCACA  
 GCCAGGGTGGCTTGTTGTTGACAGCCGCCGGCGCTCTGGCAAACCGAAAAGGATGACTGGACG  
 GTCCCTTATGGCCGCATCTACTTGGCCGGCGACACCCGCTACCGCACGGCTGGGTGGA  
 GACGGCGGTCAAGTCGGCGCTGCCGCCATCAAGATCAACAGCCGGAAAGGGCCTGCAT  
 CGGACACGGCCAGCCCCGAGGGGCACGCATCTGACATGGAGGGCAGGGCATGTGCATGG  
 GTGGCCAGCAGCCCTCGCATGACCTGGCAAAGGAAGAAGGCAGCCACCCCTCCAGTCCAAGG  
 CCAGTTATCTCTCCAAAACACGACCCACACGAGGACCTCGCAT**TAA**AGTATTTCGGAAAAAA  
 AA

## **FIGURE 50**

MAPIALHLLVLVPILLSLVASQDWKAERSQDPFEKCMQDPDYEQLLKVVTWGLNRTLKPQRV  
IVVGAGVAGLVAAKVLSAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRL  
HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKPEKLGYALRPQEKGHSPEDIYQMA  
LNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMSEDGFFYLSFAEALR  
AHSCLSDRQLQYSRIVGGWDLLPRALLSSLSGLVLLNAPVVAMTQGPHDVHVQIETSPARNL  
KVLKADVVLLTASGPRAVKRITFSPPPLPRHMQEALRRLYVPATKVFLSFRRPFWREEHIEGG  
HSNTDRPSRMIFYPPPREGALLLASYTWSAAAAFAGLSREEARLALDDVAALHGPVVRQL  
WDGTGVVKRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYRIYFAGEHTAYPHGWVETAVKS  
ALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHGVAASSPSHDLAKEEGSHPPVQGQLSLQ  
NTTHTRTS

**Signal peptide:**

amino acids 1-21

## FIGURE 51

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAACTGGGGACACTCTGGGCCGGCCTTCTGCCTGC**AT**  
**GGACGCTCTGAAGCCACCCCTGTCTGGAGGAACCACGAGCAGGGAAAGAAGGACAGGGACTCGTGTGGCAGGAA**  
 GAACTCAGAGCCGGGAAGCCCCCATTCACTAGAACGACTGAGAGATGCGGCCCGCCTCGCAGGGCTGAATTTCCT  
 GCTGCTGTTACAAGATGCTTTTATCTTAACCTTTGTTTCCCCACTTCCGACCCGGCGTTGATCTGCAT  
 CCTGACATTTGGAGCTGCCATCTTCTGTGGCTGATCACAGACCTCAACCGCTTACCTCTTGACCTGAA  
 CAATCAGTCTGTGGGAATTGAGGGAGGAGCACCGAAGGGGTTCCCAGAAGAACAAATGACCTAACAAAGTGTG  
 CTTCTCAGATGCCAAGACTATGTATGAGGTTTCCAAGAGGACTCGCTGTGTCAGAACATGGGCCCTGCTTGGG  
 ATATAGAAAACCAAACCGCCCTACAGATGGCTATCTTACAAACAGGTGTCAGTAGAGCAGAGTACCTGGGTT  
 CTGTCCTGCATAAAGGTTATAAATCATCACAGACCCAGTTGTCGGCATCTTGCTCAGAACATAGGCAGAGT  
 GATCATCTCCGAATTGGCTTGTACACGTACTCTATGGTAGCTGTACCTCTGTATGACACACCTTGGGACCAGAAC  
 CATCGTACATATTGTCAACAAGGCTGATATGCCATGGTATCTGTGACACACCCAAAAGGCATTGGTGTG  
 AGGGAAATGTAGAGAAAGGCTCACCCCGAGCCTGAAGGTGATCATCCTTATGGACCCCTTGATGATGACCTGAA  
 GCAAAGAGGGGAGAAGAGTGGAAATTGAGATCTTATCCCTATATGATGCTGAGAACCTAGGCAAAGAGCACTTCAG  
 AAAACCTGTGCCTCCTAGCCCAGAACGACTGAGCCTACAGGATCTACGATAAGGTACAAATGAGGCTAACAGG  
 AGCCATGATAACCCATCAAATATTGTTCAAATGCTGCTGCCTTCTCAAATGTGTGGAGCATGCTTATGAGCC  
 CACTCCTGATGATGTGGCCATATCCTACCTCCCTGGCTCATATGTTGAGAGGATTGTACAGGCTGTTGTGTA  
 CAGCTGTGGAGGCCAGAGTGGATTCTTCAAGGGATATTGGTTGCTGGCTGACGACATGAAGACTTGAAGCC  
 CACATTGTTCCCGCGTGCCTGACTCTTAACAGGATCTACGATAAGGTACAAATGAGGCTAACAGG  
 GAAGAAGTTCTGTTGAAGCTGGCTGTTCCAGTAAATTCAAAGAGCTCAAAAGGGTATCATCAGGCATGATAG  
 TTTCTGGGACAAGCTCATTTGCAAAGATCCAGGACAGCCTGGGCCGAAGGGTCTGTGTAATTGTCACTGGAGC  
 TGCCCCCATGTCACCTCACTGACATTCTCCGGGAGCAGGATTCGGGACTGTCAGGTGATGAAGCTTATGGTCA  
 AACAGAATGACAGGTGGCTGACATTACCTGGGACTGGACATCAGGTACGGTGGGGTGCCTGGC  
 TTGCAATTACGTGAAGCTGGAAAGATGTGGCTGACATGAACACTTACAGTGAATAATGAAGGAGAGGTCTGCAT  
 CAAGGGTACAAACGTTCAAAGGATACCTGAAGGACCTGAGAACACAGGAAGCCCTGGACAGTGTGGCTG  
 GCTTACACAGGAGACATTGGTCGCTGGCTCCGAATGGAACCTGACAGTCAACCGTAAAGAACATT  
 CAAGCTGGCCAAGGAGAATACATTGACACCAGAGATGAAAGATGAAAGCATACAGGAGTCAACCGTGTACA  
 AATTGGTACACGGGGAGAGCTACGGTACCTTAGTAGGAGTGGTGGTCTGACACAGATGACTTCCCTC  
 ATTGAGCCAAAGCTGGGTGAAGGGCTCCTTGAGGAACGTGTGACAAACAGTTGTAAGGGAGCCATT  
 AGAAGACTTGCAGAAAATGGGAAAGAAAAGTGGCTTAAACTTTGAAACAGGTCAAAGCCATTTCATCC  
 AGAGCCATTTCATTGAAAATGGGCTCTGACACCAACATTGAAAGCAAAGCGAGGAGAGCTTCCAATACTT  
 TCGGACCCAAATTGACAGCCTGTATGAGCACATCCAGGATTAGGATAAGGTACTTAAGTACCTGCCGGCCACTG  
 TGCACGTGTTGTGAGAAAATGGATTAAAAACTATTCTACATTGTTTGCCTTCCTCATTTTTTTAAC  
 TGTAAACTCTAAAGCCATAGCTTGTGTTATATTGAGACATATAATGTGAAACTTAGTCCAAATAATCA  
 ATCCGTCTTCCCCTTCATCTCGATGTTGCTAATATTAAAGGCTCAGGCTACTTTATCAACATGCCTGCTTCAA  
 GATCCCAGTTATGTTCTGTGTCCTCCTCATGATTCCAACCTTAACACTATTAGTAACCACAAGTTCAAGGGT  
 CAAAGGGACCTCTGTGCCCTCTTGTGATAAACATAACTTGCAACAGTCTCATGCTTATTACA  
 TCTTCACTGTTCAAACTAAGAGATTTAAATTCTGAAAAACTGCTTACAATTGATGTTCTAGCCACTCCAC  
 AAACCACTAAAATTGTTAGGTTAGCCTACTCATGTCATCAATCTATGAGACAAATGTCTCCGATGCTCTT  
 CTGCGTAAATTAAATTGTTGACTGAAGGGAAAAGTGTGATCATACCAACATTCTAAACTCTAGTTAGATA  
 TCTGACTTGGAGTATTAAAATTGGGTCTATGACATACTGTCAAAGGAATGCTGTTCTAAAGCATTATT  
 CAGTAGGAACCTGGGGAGTAAATCTGTTCCCTACAGTTGCTGAGCTGGAAAGCTGTGGGGAGAGTTGACA  
 GGTGGGCCAGTGAACCTTCCAGTAAATGAAGCAAGCAACTGAATAAAAACCTCTGAACACTGGGAACAAAGATCT  
 ACAGGGCAAGCAAGATGCCACACAAACAGGCTTATTCTGTGAAGGAACCAACTGATCTCCCCACCCCTGGATT  
 AGAGTTCTGCTCTACCTAACCCACAGATAACACATGTTGTTCTACTTGTAAAGTCTTAAAGTAAAC  
 TATTACAGATAAAAAAA

**FIGURE 52**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60775
<subunit 1 of 1, 739 aa, 1 stop
<MW: 82263, pI: 7.55, NX(S/T): 3
MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNFLLLFTKMLFIFN
FLFSPLPTPALICILTFGAAIFLWLITRPQPVLPLLDLNQSVGIEGGARKGVSQKNNDLTS
CCFSDAKTMYEVFQRGLAVSDNGPCLGYRKPNQPYRWLSYKQVSDRAEYLGSCLLHKGYKSS
PDQFVGIFAQNRPWEWIISELACYTYSMVAPELYDTLGPEAIVHIVNKADIAMVICDTPQKAL
VLIGNVEKGFTPSLKVIILMDPFDDDLKQRGEKSGIEILSLYDAENLGKEHFRKPVPPSPED
LSVICFTSGTTGDPKGAMITHQNIVSNAAAFLKCVEHAYEPTPDDVAISYLPLAHMFERIVQ
AVVYSCGARVGFFQGDIRLLADDMKTTLKPTLFPAPVPRLLNRIYDKVQNEAKTPLKKFLLKLA
VSSKFKELOQGIIRHDSFWDKLIFAKIQDSLGGRVRVIVTGAAPMSTSVMFFRAAMGCQVY
EAYGQTECTGGCTFTLPGDWTSGHGVGVPLACNYVKLEDVADMNYFTVNNEGEVCIKGTNVFK
GYLKDPKTQEALDSGWLHTGDIGRWLPGNTLKIIDRKKNIFKLAQGEYIAPEKIENIYNR
SQPVLQIFVHGESLRSSLGVVVVPDTDVLPSFAAKLGVKGSFEELCQNQVREAILEDLQKI
GKESGLKTFEQVKAIFLHPEPFSIENGLLPTLKAKRGELSKYFRTQIDSPLYEHQD
```

**Important features:****Type II transmembrane domain:**

amino acids 61-80

**Putative AMP-binding domain signature.**

amino acids 314-325

**N-glycosylation site.**

amino acids 102-105, 588-591 and 619-622

## **FIGURE 53**

GGAGGC GGAGGCCGCGCGAGCCGGCCGAGCAGTGAGGGCCCTAGCGGGGCCGAGCGGGG  
 CCCGGGGCCCTAAGCCATT CCTGAAGTCATGGCTGGCCAGGACATTGGTGACCCGCCAAT  
 CCGT**A**TGGACGACTGGAAGCCCAGCCCCCTCATCAAGCCCTTGGGCTCGGAAGAACGG  
 AGCTGGTACCTTACCTGGAAGTATAAACTGACAAACCAGCGGGCCCTCGGGAGATTCTGTCA  
 GACAGGGCCGTGCTTTCTGCTGGTACTGTCAATTGCAATATCAAGTTGATCCTGGACA  
 CTGGCGAGCCATCAGTGAAGCCAATGAAGACCCAGAGCCAGAGCAAGACTATGATGAGGCC  
 CTAGGCCGCTGGAGCCCCACGGCGCAGAGGCAGTGGTCCCCGGCGGGTCTGGACGTAGA  
 GGTGTATTCAAGTCGCAGCAAAGTATATGTGGCAGTGGATGGCACCGTGCTGGAGGATG  
 AGGCCGGGAGCAGGGCCGGGCATCCATGTCATTGTCCTCAACCAGGCCACGGGCACGTG  
 ATGGAAAACGTGTGTTGACACGTACTCACCTCATGAGGATGAGGCCATGGTGTATTCT  
 CAACATGGTAGCGCCCGGGCAGTGCTCATCTGCACTGTCAAGGATGAGGCCCTTCCACC  
 TCAAGGACACAGCCAAGGCTCTGCTGAGGAGCCTGGCAGCCAGGCTGGCCTGCCCTGGC  
 TGGAGGGACACATGGCCTCTGGAGAAAAGGAGGTCTGTCTCGGGAGAAACATTC  
 TAAGTCACCTGCCCTCTTCCCTGGGGGACCCAGTCCTGCTGAAGACAGATGTGCCATTGA  
 GCTCAGCAGAAGAGGCAGAGTGCCACTGGCAGACACAGAGCTGAACCGTCGCCGGCGC  
 TTCTGCAGCAAAGTTGAGGGCTATGGAAGTGTATGCAGCTGCAAGGACCCACACCATCGA  
 GTTCAGCCCTGACCCACTCCCAGACAACAAGGTCTCAATGTGCCGTGGCTGTCAATTGCAG  
 GGAACCGACCCAATTACCTGTACAGGATGCTGCCCTCTGCTTCAGGCCAGGGGTGTCT  
 CCTCAGATGATAACAGTTTCAATTGACGGCTACTATGAGGAACCCATGGATGTGGTGGCACT  
 GTTGGTCTGAGGGCATCCAGCATACTCCCATTGACATCAAGAATGCCCGTGTCTCAGC  
 ACTACAAGGCCAGCCTCACTGCCACTTCAACCTGTTCCGGAGGCCAAGTTGCTGTGGTT  
 CTGGAAGAGGACCTGGACATTGCTGTGGATTTCAGTTCTGAGCCAATCCATCCACCT  
 ACTGGAGGAGGATGACAGCCTGTACTGCATCTGCCTGGAATGACCAGGGTATGAAACACA  
 CGGCTGAGGACCCAGCACTACTGTACCGTGTGGAGACCATGCCCTGGCTGGCTGGGTGCTC  
 AGGAGGTCTGTACAAGGAGGAGCTTGAGGCCAAGTGGCTACACCGGAAAAGCTCTGGGA  
 TTGGGACATGTGGATGCGGATGCCCTGAACAACGCCGGGCGAGAGTGCATCATCCCTGACG  
 TTTCCGATCCTACCACTTGGCATCGTCGGCTCAACATGAATGGCTACTTTCACGAGGCC  
 TACCTCAAGAAGCACAAGTTCAACACGGTCCAGGTGTCAGCTCAGGAATGTGGACAGTCT  
 GAAGAAAGAAGCTTATGAAGTGGAAAGTTCACAGGCTGCTCAGTGGAGGCTGAGGTTCTGGACC  
 ACAGCAAGAACCCCTGTGAAGACTCTTCCCTGCCAGACACAGAGGCCACACCTACGTGGCC  
 TTTATTGCAATGGAGAAAGATGATGACTTCACCACCTGGACCCAGCTGCCAAGTGCCTCCA  
 TATCTGGGACCTGGATGTGCGTGGCAACCCTGGGGCTGTGGAGATTGTTCGGAAGAAGA  
 ACCACTCCTGGTGGTGGGGTCCCGCTTCCCTACTCAGTGAAGAACGCCACCCCTAGTC  
 ACCCCAAATTTCCTGGAGGCCACCCCAAAGGAGGAGGGAGGCCAGGAGGCCAGAACAGAC  
**A**TGA GACCTCCTCCAGGACCCCTGCAGGGCTGGTACTGTGTAACCCAGGCTGGCTAGCCCT  
 TCCCTCCATCCTGTAGGATTTGTAGATGCTGGTAGGGCTGGCTACCTTGTGTTTAACA  
 TGAGACTTAATTACTAACCAAGGGAGGGTCCCTGCTCCAACACCCGTTCTGAGTT  
 AAAAGTCTATTATTACTTCCCTGTTGGAGAAGGGCAGGAGAGTACCTGGGAATCATTACG  
 ATCCCTAGCAGCTCATCCTGCCCTTGAATACCCCTACTTCCAGGCCTGGCTCAGAATCTA  
 ACCTATTATTGACTGTGCTGAGGGCCTTGAAAACAGGCCGAACCTGGAGGGCTGGATTTC  
 TTTTGGGCTGGAATGCTGCCCTGAGGGTGGGCTGGCTTACTCAGGAAACTGCTGTGCC  
 CAACCCATGGACAGGCCAGCTGGGGCCACATGCTGACACAGACTCACTCAGAGACCCTA  
 GACACTGGACCAGGCCCTCTCAGCCTCTTGTCCAGATTCAAAGCTGGATAAGTT  
 GGTCAATTGATTAAGGAGAAGCCCTCTGGAAAAA

## **FIGURE 54**

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA61185
>subunit 1 of 1, 660 aa, 1 stop
><MW: 75220, pI: 6.76, NX(S/T): 0
MDDWKPSPLIKPFGARKKRSWYLTWKYKLTNQRALRRFCQTGAVLFLLVTIVNIKLILDTR
RAISEANEDPEPEQDYDEALGRLEPPRRRGSGPDRVLDVEVYSSRSKVVAVDGTTVLEDEA
REQRGRIHVIVLNQATGHVMAKRVFDTYSYPHEDEAMVLFLNMVAPGRVLICTVKDEGSFHLK
DTAKALLRSLGSQAGPALGWRDTWAFVGRKGKPVGKHSKSPALSSWGDPVLLKTDVPLSS
AEEAECHWADTELNRRLRFCSKVEGYGSVCSCDKPTPIEFSPDPLPDNKVLNPVAVIAGN
RPNLYRMLRSLLSAQGVSPQMITVFIDGYEEMDVALFGLRGIQHTPISIKNARVSQHY
KASLTATFNLFPEAKFAVVLEEDLDIAVDFSFLSQSIIHLLEEDDSLYCISAWNDQGYEHTA
EDPALLYRVETMPGLGWVLRRSLYKEELEPKWPTPEKLWDWDMWMRMPEQRRGRECIIPDVS
RSYHFGIVGLNMNGYFHEAYFKKHKFNTVPGVQLRNDSLKKEAYEVHRLLSEAEVLDHS
KNPCEDSFLPDTEGHTYVAFIRMEKDDDFTTWTQLAKCLHIWDLDVRGNHRGWLFRKKNH
FLVVGVPASPYSVKKPPSVTPIFLEPPPKEEGAPGAPEQT
```

**Important features of the protein:**

**Transmembrane domain:**

amino acids 38-55

**Homologous region to Mouse GNT1**

amino acids 229-660

## FIGURE 55

CGGACGCGTGGCTGGTGGAAAGCCTAAAGAACGAACTGGAAAGCCACTCTCTTGGAACCAACAC  
 CTGTTAAAGAACCTAACGACCATTAAAGCCACTGGAAATTGTTGTCTAGTGGTGTGGGTGAATA  
 AAGGAGGGCAGA**ATGG**ATGATTCTCATCTCATTAGCCTGCTGTCTGGCTATGTTGGTGGGATGTTA  
 CGTGGCCGGAATCATTCCCTGGCTGTTAATTCTCAGAGGAACGACTGAAGCTGGTACTGTTTGG  
 GTGCTGGCCTCTCTGTGGAACGTGCTGTGCAGTCAGTGCCTGAAGGAGTACATGCCCTTATGAA  
 GATATTCTTGAGGGAAAACACCAAGCAAGTGAACACATAATGTGATTGCATCAGACAAAGCAGC  
 AGAAAAATCAGTTGTCATGAACATGAGCACGCCACACAGCTGCATGCCTATATTGGTG  
 TTTCCCTCGTCTGGGCTCGTTTCATGTTGCTGGTGGACCAGATTGTAACCTCCATGTGCATTCT  
 ACTGACGATCCAGAACGAGCAAGGTCTAGCAATTCAAACATCACCACCGCTGGGTCTGGGTGTCCA  
 TGCTGCAGCTGATGGTGTGCTTGGGAGCAGCAGCATCTACACAGACAGTGTCCAGTTAATTG  
 TGTTGTGGCAATCATGCTACATAAGGCACCAGCTGCTTTGGACTGGTTCTTGTGATGCATGCT  
 GGCTTAGAGCGGAATCGAACAGAACACTGCTGGTCTTGCAATTGGCAGCACAGTTATGTCCAT  
 GGTGACATACTTAGGACTGAGTAAGAGCAGTAAAGAACGCCCTTCAGAGGTGAACGCCACGGGAGTGG  
 CCATGCTTTCTCTGCCGGACATTCTTATGTTGCCACAGTACATGTCCTCCCTGAGGTGGCGGA  
 ATAGGGCACAGCCACAAGCCGATGCCACGGGAGGGAGAGGCCTCAGGCCCTGGAAGTGGCAGCCCT  
 GGTTCTGGGTGCCTCATCCCTCATCCCTGTCAGTAGGACACCAGCAT**TAA**ATGTTCAAGGTCCAGC  
 CTTGGTCCAGGGCCGTTGCCATCCAGTGAGAACAGCCGGCACGTGACAGCTACTCACTCCTCAGTC  
 TCTTGTCTCACCTGCGCATCTACATGTATTCTAGAGTCCAGAGGGGAGGTGAGGTTAAAACCTG  
 AGTAATGGAAAAGCTTTAGAGTAGAACACATTACGTTGCAAGTTAGCTATAGACATCCCATTGTG  
 TATCTTTAAAAGGCCCTGACATTTGCGTTTAATATTCTCTTAACCTATTCTCAGGGAAAGATG  
 GAATTAGTTAAGGAAAAGAGGAGAACCTCATACTCACAATGAAATAGTGATTATGAAAATACAGT  
 GTTCTGTAATTAGCTATGCTCTTCTTAGTTAGAGGCTGCTACTTATCCATTGATT  
 AACATGGTTCCCACCATGTAAGACTGGTGCTTAGCATCTATGCCACATGCGTTGATGGAAGGTATA  
 GCACCCACTCACTTAGATGCTAAAGGTGATTCTAGTTAATCTGGGATTAGGGTCAGGAAAATGATAGC  
 AAGACACATTGAAAGCTCTTTACTCAAAAGAGATATCCATTGAAAAGGGATGTCTAGAGGGATT  
 TAAACAGCTCTTGGCACGTGCCCTCTGAATCCAGCCTGCCATTCCATCAAATGGAGCAGGAGAGG  
 TGGGAGGAGCTCTAAAGAGGTGACTGGTATTTGTTAGCATTCTGTCAAGTTCTCCTTGCGAGAAT  
 ACCTGTCCTCACATTCTAGAGAGGAGCCAAGTTCTAGTTCTAGGCTTCTTCAGAA  
 CAGTCAGATCACAAAGTGTCTTGGAAATAAGGGATATTAAATTAAAGTGA  
 TGATATCTTGTAGCTTTTTAAAGACTACCAAAATGTATGGTGTCTTTTTGTT  
 TTTTTTTAATTATTCTCTTAGCAGATCAGCAATCCCTCTAGGGACCTAAATACTAGGTCACT  
 GGCGACACTGTGCTCTCACATAACCACCTGCTAGCAAGATGGATCAAATGAGAAGTGTGCTA  
 TTGATTAAAGCTTATGGAATCATGTCCTGTCTTCGTCTTGTCTTCTTCTA  
 TCCCTCTAGCCTCTGCCACAATTGCTGCTACTGCTGGTGTAAATTGTTGTTG  
 CTTATCAGGACAACCACCTCTGAACTGTAATAATGAAGATAATAATCTTATCTT  
 CAAAGAAATTACCTTGTGTCAAATGCCCTTGTGAGCCCTAAACACCACCTCT  
 ATTGACACAATCACTAATCTGGTAATTAAACAATTGAGATAGCAGGAAAGTGT  
 ATTGTTCTTGCATATTGCCAAATTGTTGAAACCCCTGTCTGTCAAATAAGTGT  
 TATAATTATTACTTCTATACCATTCAAAACACATTACACTAAGGGGAACCAAGACTAGTT  
 TCTCAGGGCAGTGGACGTAGTAGTTGTAACAGCTTCTATGACGCTAGCATGCCTATG  
 ATTATTCTTCTCATGAATTGTCAGGGATCAGCAGCTGTGGAATAAGCTTGT  
 GGCCACAGTGAGGAAAGTAGCAGAACATAGGATACAGTTGTTAGTCATTGG  
 ATTTACTACCAAGAGAAGGTAGTATGAAAGTCAAATGACTCCTGATTGGATG  
 GACTGGTGTGAGACTTGAGGTTCATCTAGCTTCAAAACTATATGGTGCCTAGATTCTCT  
 AACTGACTTTGTCAAATAAGCAGATTGTTAGTGTCAAAAAAAA

## **FIGURE 56**

MDDFISISLLSLAMLVGCYVAGIIPLAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHAL  
YEDILEGKHHQASETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVFMLLVDO  
IGNSHVHSTDDPEAARSSNSKITTLGLVVHAAADGVALGAAASTSQTSQLIVFVAIMLHK  
APAAFGLVSFLMHAGLERNRIRKHLVFAAAPVMSMVTYLGLSKSSKEALSEVNATGVAML  
FSAGTFLYVATVHVLPEVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPLIISVGHQH

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 37-56, 106-122, 211-230, 240-260, 288-304

**FIGURE 57**

GCTCGAGGCCGGCGGCGGGAGAGCGACCCGGCGGCCTCGTAGCGGGGCCGGATCCC  
CGAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTTGAGATGATGGGCTTGG  
GAAACGGCGTCGCAGCATGAAGTCGCCGCCCTCGTGTGGCCGCCCTGGTGGCCTGCATC  
ATCGTCTTGGGCTTCAACTACTGGATTGCGAGCTCCGGAGCGTGGACCTCCAGACACGGAT  
CATGGAGCTGGAAGGCAGGGTCCGCAGGGCGGCTGCAGAGAGAGGGCGCCGTGGAGCTGAAGA  
AGAACGAGTTCCAGGGAGAGCTGGAGAAGCAGCAGGGAGCAGCTTGACAAAATCCAGTCCAGC  
CACAACTCCAGCTGGAGAGCGTCAGAACAGCTGTACCAGGACGAAAAGGCGTTTGGTGAA  
TAACATCACACAGGTGAGAGGGCTCATCCGAGTGCTGCAAGACCAGTTAAAGACCCCTGCAGA  
GGAATTACGGCAGGCTGCAGCAGGATGTCCTCCAGTTCAAAGAACAGACCAACCTGGAG  
AGGAAGTTCTCCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTG  
TGAGGAGCGAATAGAAGAGGTACCAAAAAGGGAATGAAGCTGTAGCTTCAGAGACCTGA  
GTGAAAACAACGACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAG  
GCAGCAGGCCCTGCCACACACAGAGGTGCCACAAGGGAAACGTGCTTGGTAACAGCAA  
GTCCCAGACACCAGCCCCAGTTCCGAAGTGGTTTGGATTCAAAGAGACAAAGTTGAGAAAG  
AGGAAACCAATGAGATCCAGGTGGTAATGAGGAGCCTCAGAGGGACAGGCTGCCGCAGGAG  
CCAGGCCGGGAGCAGGTGGTAAGACAGACCTGTAGGTGGAAAGAGGCTCGGGGAGCCGG  
AGAACTGGGCCAGACCCCACAGGTGCAGGCTGCCCTGTCAGTGAGCCAGGAAAATCCAGAGA  
TGGAGGGCCCTGAGCGAGACCAGCTTGTCAATCCCCGACGGACAGGAGGAGCAGGAAGCT  
GCCGGGAAGGGAGAAACCAGCAGAAACTGAGAGGGAGAAGATGACTACAACATGGATGAAAA  
TGAAGCAGAATCTGAGACAGACAAGCAAGCAGCAGCCCTGGCAGGGAAATGACAGAAACATAGATG  
TTTTAATGTTGAAGATCAGAAAAGAGACACCATAAATTACTTGATCAGCGTGAAAAGCGG  
AATCATAACTCTGAATTGAACGTGGAAATCACATATTCACAACAGGGCGAAGAGATGACTA  
TAAAATGTTCATGAGGGACTGAATACTGAAAATGTACTAAATAATGTACATCTGA

## **FIGURE 58**

MMGLGNRGRSMKSPPVLAALVACIIVLGFNYWIASSRSVLDLQTRIMELEGRVRRAAAERGA  
VELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLQYQDEKAVLVNNITTGERLIRVLQDQL  
KTLQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVA  
SRDLSENNDQRQQLQALSEPQPRLQAAGLPHTEPQGKGNVLGNSKSQTPAPSSEVVLDSKR  
QVEKEETNEIQVVNEEPQRDRLPQEPMREQVVEDRPVGGRGF GGAGELGQTPQVQAALSVSQ  
ENPEMEGPERDQLVIPDGQEEEQEAAGEGRNQQKLRGEDDYNMDENEAESETDKQAALAGND  
RNIDVFNVEDQKRDTINLLDQREKRNHTL

**Signal peptide:**

amino acids 1-29

## FIGURE 59

**GGATGCAGAAAGCCTCAGTGTGCTTCCTGGCCTGGGCTGTTCTCTACGCTGGCATTGCCCTTTCA**  
 CCAGTGGCTTCCTGCTCACCGTTGGAGCTCACCAACCATAAGCAGCTGCCAAGAGCCCCAGGCCCTGGTCCC  
 TGCCATGGGGAGCCAAGGAAACCTGGGCTGCTGGATGGCTCCGATTTCGCGGGTTGTGTTGGCTGA  
 TAGATGCTCTGCGATTGACTTCGCCAGCCCCAGCATTACACGTGCCCTAGAGAGCCTCTGTCTCCCTACCCCT  
 TCCTGGGCAAACATAAGCTCTTGCAAGGAGATCCTGGAGATTAGCCCCACCATGCCCGCTCTACCGATCTCAGG  
 TTGACCCCTCCTACCAACCATGCAGGCCCTCAAGGCCCTCACCACTGGCTACTGCCCTACCTTATTGATGCTG  
 GTAGTAACCTGCCAGGCCACGGCATAGTGGAAAGACAATCTCATTAAGCAGCTCACCAGTGCAGGAAGGCGTAG  
 TCTTCATGGGAGATGATACTGGAAAGACCTTCCCTGGTCTTCTCAAAGCTTCTTCTCCATCCTCA  
 ATGTCAGAGACCTAGACACAGTGGACAATGGCATCCTGGAACACCTCACCCACCATGGACAGTGGTAATGGG  
 ACGTGCTGATTGTCACTTCTGGGTGTGGACACTGTGCCACAAGCATGCCCTCACCAACCTGAAATGCCA  
 AGAAACTTAGCCAGATGGACCAAGGTGATCCAGGGACTTGTGGAGCGTCTGGAGAATGACACACTGCTGGTAGTGG  
 CTGGGACCATGGGATGACCAACAAATGGAGACCATGGAGGGACAGTGGAGCTGGAGGTCTAGCTGCTCTTT  
 TGTATAGCCCCACAGCAGTCTTCCCCAGCACCCACAGAGGGAGCCAGAGGTGATTCTCAAGTTAGCCTGTGC  
 CCACGCTGGCCCTGCTGGGCTGCCATCCCATTGGAATATCGGGAAAGTGTGAGCTGAGCTATTCTCAG  
 GGGGTGAGGACTCCCAGCCCCACTCCTCTGCTTAGCCAAGCCTCAGCTCTCATCAATGCTCAGCAGGTGT  
 CCCGATTTCTTCATACCTACTCAGCTGACTCAGGACCTCAAGCTAAGGAGCTTCAGCTGCAGAACCTCT  
 TCTCCAAGGCCCTGCTGACTACCAGTGGCTTCTCCAGAGCCCCAAGGGGGCTGAGGCAGACTGCCACTGTGA  
 TTGCTGAGCTGCAGCTCTGCCAGCTGGGAGCTGGCCATGTGCATCAGTCTGGCTCGTTCTCTGGTCC  
 GCATGGCGGGGGTACTGCTCTTGGCTGCTTATCTGCTGCTGGCATCTCAGTGGCAATATCCC  
 CAGGCTTCCATTCTGCCCTACTCCTGACACCTGTGGCTGGGCTGGTTGGGCCATAGCTATGCTGGAC  
 TCCTGGGAACTATTGAGCTGAAGCTAGATCTAGTGTCTAGGGCTGTGGCTGCAGTGAAGCTCATTCTCCCTT  
 TTCTGTGAAAGCCTGGCTGGCTGGGCTCAAGAGGCCCTGGCAACCCCTGTTCCCATCCCTGGGCCGTCC  
 TGTTACTCCTGCTGTTGCTTGGCTGTGTTCTCTGATAGTTGTTAGCTGAGGCCAGGGCACCCCT  
 TCCTTTGGGCTCATTCTGCTCTGGTGTCCAGCTTCACTGGAGGGCCAGCTGCTTCCACCTAACCTAC  
 TCACAATGCCCGCCCTGGCACTTCAGCCACAAACAAACCCCCACGGCACAATGGCATATGCCCTGAGGTTG  
 GAATTGGGTTGCTTTATGTACAAGGCTAGCTGGCTTTTATGGTGCATGGCTGAGAGACACCTGTTGCACT  
 CCTCTCCCTGGCTGAGTCTCTGGCATTGGTGGTGTGAGCCAAGAATTATGGTATGGAGCTGTTG  
 CGGCCCTGGTGGCCCTGTAGCTCCCGTGCCTGGCTTGGCTCGCCGCTATGGTAACTCAAGAGCCCCAGGCCAC  
 CCATGCTCTTGTGCGCTGGGACTGCCCCATAATGGCATTGGTACTGCTGCCTACTGGCATTGGCTGGGG  
 CAGATGAGGCTCCCCCGCTCCGGTCTGGCTCTGGGCTGACAGTGTGGTAAGGCTGGGCAGGGCTCCAA  
 TGGCTGCTTCAAGGCTCGCCTGCTGCTCTGGAGCTGACAGTGTGGTAAGGCTGGGCAGGGCTCCAA  
 GGACCAAGACTGTCCTCACTCCCTCTCAGGCCCTTCAAGCTGACTGGATTATGTGGCTCTCAA  
 TCTACCGACACATGCAGGAGGAGTCCGGGCGGTTAGAGAGGACAAATCTCAGGGTCCCTGACTGTGGCTG  
 CTTATCAGTTGGGAGTGTCTACTCAGCTGCTATGGTCACAGCCCTACCCCTGTTGGCTTCCCACCTCTGCTG  
 TGCTGCGAGCGCATCAGCCTTGTGTTCTGCTTCTGCTGAGCTCCCTCCTACATCTGCTGCTG  
 CTGGGATACCGTCACCAACCCCTGGCTTTACTGTGCATGGCAGGAGTCTCGGCTGGCCCTCATGGCCA  
 CACAGACCTACTCCACAGGCCACCAGCCTGCTTCCAGCCATCCATTGGCATGCAGCCCTGTTGGGATTCC  
 CAGAGGGCATGGCTCTGACTTGGCTGCCCTTGCTAGTGGAGGCAACACCTTGCCTCCACCTCT  
 TTGAGTAGGTTGCCACTGCTCTGCTCTGGCTTCTGTTGAGAGTCAAGGGCTGCCAGAGACAGCAGC  
 CCCAGGGAAATGAAGCTGATGCCAGAGTCAGACCCGAGGGAGGAAGAGGAGGCCACTGATGGAGATGCC  
 ATGCGCCTCAGCACTTCTATGCAGCACTGCTGCCAGGCCCTAAGTACCTCTTATCTGGTATTCA  
 TGGGCTGTGCCCTGGCAGGCCATCCTCTGCAAGGCATCTCATGGTCTGGAAAGTGTGTTGGCC  
 TAAGTTCAATTGAGGCTGTTGAGAGTGGATGAGAGTGGATGGT  
 CTGTGAGCTCTGGTTCAGGCAGCTATTCTGGCCAGCAGGATTAGCTGCTGATTACTGGCATTGGCT  
 ACAGAGAGTGTGGAGAACAGTGTAGCCTGGCCTGTACAGGTAAGTGTGATCTGCAAGACAGGCTGCC  
 ATACCTTACTATCATGCAGCCAGGGCCGCTGACATCTAGGACTTCATTATTCTATAATT  
 CAGGACCAAGTGGAGTA  
 TGATCCCTAACTCCTGATTGGATGCATCTGAGGGACAAGGGGGCGGTCTCGGAAGTGGAAATAA  
 ATAGGCCGG  
 GCGTGGTGAATTGCACCTATAATCCAGCACTTGGGAGGCAGAGGTGGGAGGATTGCTTGGTCCCAGGAGTTCA  
 AGACCAGCCTGTGAAACATAACAAGACCCGCTCTACTATTAAAAAAAGTGAATAAAATGATAATAT

## **FIGURE 60**

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809
<subunit 1 of 1, 1089 aa, 1 stop
<MW: 118699, pI: 8.49, NX(S/T): 2
MQKASVLLFLAWVCFLFYAGIALFTSGFLTRLELTNHSSCQEPPPGPSLPWGSQGKPGACW
MASRFSRVVLVLIDALRFDFAQPOQHSHVPREPPVSLPFLGKLSSIQRILEIQPHHARLYRSQ
VDPPTTMQRLKALTGSLPTFIDAGSNFASHAIVEDNLIKQLTSAGRVVFMGDDTWKDLF
PGAFSKAFFFPSFNVRDLDLTVNGILEHLYPTMDSGEWDVLIAHFLGVDHCGKHGPHEM
AKKLSQMDQVIQGLVERLENDTLLVVAGDHGMTTNGDHGGDSELEVSAALFLYSPTAVFPST
PPEEPEVIPQVSLVPTLALLLGLPIPFGNIGEVMAELFSGGEDSQPHSSALAQASALHLNAQ
QVSRLFHTYSAATQDLQAKELHQQLQNLFSKASADYQWLLQSPKGAEATLPTVIAELQQFLRG
ARAMCIESWARFSLVRMAGGTALLAASCFCILLASQWAISPGFPFCPLLLTPVAWGLVGAIA
YAGLLGTIELKLDLVLLGAVA AVSSFLPFLWKAWAGWGSKRPLATLFPPIP GPVLLLLFRLA
VFFSDSFVVAEARATPFLGSFILLLVQLHWEGQLLPPKLLTMRPLGTSATTNPPRHNGAY
ALRLGIGLLLCTRLAGLFHRCPEETPVCHSSPWLSPLASMVGGRAKNLWYGACVAALVALLA
AVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPPRLRVLVSGASMVLP
RAVAGLAASGLALLIWKPVTVLVKAGAGAPRTRTLTFSGPPTSQADLDYVVPQIYRHMQE
EFRGRLERTKSQGPLTVAAYQLGSVYSAAMVTALTLLAFPLLLHAERISLVFLLLFLQSFL
LLHLLAAGIPVTTPGPFTVPWQAVSAWALMATQTFYSTGHQPVFPAIHWAAFVGPEGHGS
CTWLPALLVGANTFASHLLFAVGCPLLLWPFLCESQGLRKRQQPPGNEADARVRPEEEEP
LMEMRLRDAPQHFYAALLQLGLKYLFI LGI QILACALAASI LRRHLMVWKVFAPKFIFEAVG
FIVSSVGLLGLIALVMRVDGAVSSWFRQLFLAQQR

```

**Important features:****Signal peptide:**

amino acids 1-16

**Transmembrane domains:**amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850,  
1016-1034, 1052-1070**Leucine zipper pattern.**

amino acids 843-864

**N-glycosylation sites.**

amino acids 37-40, 268-271

## **FIGURE 61**

TGCCCGCTGCCGCCGCTGCTGCTGGCTCCTGGCGGCCTGGGGACGGGCAGTCCCTGT  
GTCTCTGGTGGTTGCCTAACACTGCAAACATCACCTCTTATCCATCAACATGAAGA**ATGT**  
CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATT  
TCATCACAAATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTCTGTTGT  
CCTGACAGCTCCAGAGAAGTGGAGAGAAATCCAGAAGACCTCCTGTTCCATGCAACAAA  
TATACTCCAATCTGAAGTATAACGTGTCTGTTGAATACTAAATCAAACAGAACGTGGTCC  
CAGTGTGTGACCAACCACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTACTGCCT  
ACACGTGGAGTCCTCGTCCCAGGGCCCCCTGCCGTGCTCAGCCTCTGAGAAGCAGTGTG  
CCAGGACTTGAAGATCAATCATCAGAGTTCAAGGCTAAATCATCTCTGGTATGTTTG  
CCCATATCTATTACCGTGTCTTTCTGTGATGGGCTATTCCATCTACCGATATATCCA  
CGTTGGCAAAGAGAAACACCCAGCAAATTGATTTGATTATGAAATGAATTGACAAAA  
GATTCTTGTGCCGTGCTGAAAAAATCGTATTAACCTTATCACCTCAATATCTCGGATGAT  
TCTAAAATTCTCATCAGGATATGAGTTACTGGAAAAAGCAGTGATGTATCCAGCCTAA  
TGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTAG  
GGTATGCTCGCATTGATGGAAATTCTGTGACTCTGAAGAAAACACGGAAGGTACTTCT  
CTCACCCAGCAAGAGTCCCTCAGCAGAACAAATACCCCCGGATAAAACAGTCATTGAATATGA  
ATATGATGTCAGAACCACTGACATTGCGGGGCTGAAGAGCAGGAGCTCAGTTGCAGG  
AGGAGGTGTCCACACAAGAACATTATTGGAGTCGCAGGCAGCGTTGGCAGTCTGGGCCG  
CAAACGTTACAGTACTCATACACCCCTCAGCTCAAAGACTTAGACCCCTGGCGCAGGAGCA  
CACAGACTCGGAGGAGGGCCGGAGGAAGAGCCATCGACGACCCCTGGTCAGTGGATCCCC  
AAACTGGCAGGCTGTGATTCTCGCTGTCAGCTCGACCAGGATTCAAGGGCTGCGAG  
CCTCTGAGGGGATGGCTCGGAGAGGGTCTCTATCTAGACTCTATGAGGAGGCCG  
TCCAGACAGGCCACCAGGAGAAATGAAACCTATCTCATGCAATTCAAGGGGATGGGGT  
TATATGTGCAGATGGAAA**TGA**TGCCAACACTCCCTTGCCTTGTGAAAC  
AAAGTGAAGTCACCCCTTGATCCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTCCAGT  
TTGTCAGTGTGTGAGAATTACTTATTCTCTATTCTCATAGCACGTGTGATTG  
GTTCATGCATGTAGGTCTCTAACATGATGGTGGCCTCTGGAGTCCAGGGCTGGCCGGT  
TGTTCTATGCAGAGAAAGCAGTCAATAATGTTGCCAGACTGGGTGCAGAATTATTATTCAAGG  
TGGGTGT

## FIGURE 62

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815
<subunit 1 of 1, 442 aa, 1 stop
<MW: 49932, pI: 4.55, NX(S/T): 5
MSYNGLHQRFKELKLLTLCISISSQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQ
QIYSNLKYNVSVLNTKSRTWSQCVTNHTLVLTWLEPNLTYCVHVESFVPGPPRRAQPSEKQ
CARTLKQDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILYGNEDF
KRFFVPAEKIVINFITLNISDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEVKH
LGYASHLMEIFCDSEENTEGTSLTQQESLSRTIPPDKTVIEYEYDVRTTDICAGPEEQELSL
QEEVSTQGTLLSQAAALAVLGPQLQSYTPQLQDLDPLAQEHTDSEEGPEEEPSTTLVDWD
PQTGRLCIPSLSSFDQDSEGCEPSEGDSLGEEGLLSRLYEEPAPDRPPGENETYLMQFMEEW
GLYVQmen
```

**Important features:**

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 140-163

**N-glycosylation sites.**

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

**FIGURE 63**

CGGACGCGTGGCGGACGCGTGGCGGACGCGTGGGTCTCTGCAGGGAGACGCCAGCCTGCG  
TCTGCC**ATG**GGGCTCGGGTTGAGGGCTGGGACGTCCCTGCTGACTGTGCCACGCCCT  
GATGCTGCCGTGAAGCCCCCGCAGGCTCCTGGGGGCCAGATCATGGGGGCCACGAGG  
TGACCCCCCACTCCAGGCCCTACATGGCATCCGTGCGCTTCGGGGCCAACATCACTGCGA  
GGCTTCCTGCTGCGAGCCCCTGGGTGGTCTCGGCCGCCACTGCTTCAGCCACAGAGACCT  
CCGCACGGCCTGGTGGTGCTGGCGCCACGTCCCTGAGTACTGCGGAGCCCACCCAGCAGG  
TGTTTGGCATCGATGCTCTCACACGACCCGACTACCACCCATGACCCACGCCAACGAC  
ATCTGCCTGCTGCGCTGAACGGCTCTGCTGTCCTGGGCCCTGCAGTGGGCTGCTGAGGCT  
GCCAGGGAGAAGGGCAGGCCACAGGGGGACACGGTGCCGGTGGCTGGCTGGGCT  
TCGTGTCTGACTTTGAGGAGCTGCCCTGGACTGATGGAGGCCAAGGTCCGAGTGCTGGAC  
CCGGACGTCTGCAACAGCTCCTGGAAGGGCACCTGACACTTACCATGCTCTGCACCCGAG  
TGGGGACAGCCACAGACGGGCTTCTGCTGCCGACTCCGGAGGGCCCTGGTGTGCAGGA  
ACCGGGCTCACGCCCTGTTCTCGGGCCTCTGGTGCGGGACCCCAAGACCCCGAC  
GTGTACACGCAAGGTGTCGCCCTTGATCTGGGACGTGGTTCGGCAGCAGTCC  
CCAGCCCCGGCCCTGCCTGGGACCACCAAGGCCCCAGGAGAAGCCGCC**TGA**GCCACAACCT  
TGGGGCATGCAAATGAGATGCCGCTCCAGGCCTGGAATGTTCCGTGGCTGGGCCCCACGGG  
AAGCCTGATGTTCAAGGGTTGGGTGGGACGGGAGCGGGCACACCCATTCCACATGCA  
AAGGGCAGAAGCAAACCCAGTAAATGTTAACTGACAaaaaaaaaaaaaAGAAA

## **FIGURE 64**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845
><subunit 1 of 1, 283 aa, 1 stop
><MW: 30350, pI: 9.66, NX(S/T): 2
MGLGLRGWGRPLLTVALMLPVKPPAGSWGAQIIGGHEVTPHSRPYMASVRFGGQHHCGGF
LLRARWVVSAAHCFSHRDLRTGLVVLGAHVLSTAEPQQVFGIDALTTHPDYHPMTHANDIC
LLRLNNGSAVLGPAVGLLRLPGRARRPPTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPD
VCNSSWKGHLTLMCTRSGDSHRRGFCASADSGGPLVCRNRAHGLVSFSGLWC GDPKTPDVY
TQVSAFVAWIWDVVRRSSPQPGPLPGTTRPPGEAA
```

**Signal peptide:**

amino acids 1-30

## **FIGURE 65**

GAGCTACCCAGGCGGCTGGTGTGCAGCAAGCTCCGCGCCACTCCGGACGCCGTACGCCCTGA  
 CGCCTGTCCCCGGCCCGGCATGAGCCGCTACCTGCTGCCGCTGTCGGCGCTGGGCACGGTAG  
 CAGGCGCCGCCGTGCTCAAGGACTATGTCACCGGTGGGCTGCCCCAGCAAGGCCACC  
 ATCCCTGGGAAGACGGTCATCGTGACGGCGCCAACACAGGCATCGGGAAAGCAGACCGCCTT  
 GGAACCTGCCAGGAGAGGAGGCAACATCATCCTGGCCTGCCAGACATGGAGAAGTGTGAGG  
 CGGCAGCAAAGGACATCCGCGGGAGACCCCTCAATCACCATGTCAACGCCGGCACCTGGAC  
 TTGGCTTCCCTCAAGTCTATCCGAGAGTTGCAGCAAAGATCATTGAAGAGGGAGGAGCGAGT  
 GGACATTCTAACACAACGCGGGTGTGATGCGGTGCCACTGGACCAACGAGGACGGCT  
 TCGAGATGCAGTTGGCGTTAACACCACCTGGTCACTTCTCTTGACAAACTTGCTGCTGGAC  
 AAGCTGAAAGCCTCAGCCCCTCGCGGATCATCAACCTCTCGTCCCTGCCCATTTGCTGCTGG  
 GCACATAGACTTTGACGACTTGAACGGCAGACGAGGAAGTATAAACACCAAAGCCGCCTACT  
 GCCAGAGCAAGCTGCCATCGCCTCTCACCAAGGAGCTGAGCCGGCGCTGCAAGGCTCT  
 GGTGTACTGTCAACGCCCTGCACCCGGCGTGGCCAGGACAGAGCTGGCAGACACACGGG  
 CATCCATGGCTCCACCTTCTCAGCACCAACTCGGGCCCATCTCTGGCTGCTGGTCAAGA  
 GCCCGAGCTGCCGCCAGCCCAGCACATACCTGGCGTGGCGAGGAACGGCGGATGTT  
 TCCGGAAAGTACTCGATGGACTCAAACAGAAGGCCCCGGCCCCGAGGCTGAGGATGAGGA  
 GGTGGCCCGGAGGCTTGGCTGAAAGTGCCGCCTGGTGGCTTAGAGGCTCCCTGTGA  
 GGGAGCAGCCCTCCCCAGATAACCTCTGGAGCAGATTGAAAGCCAGGATGGCGCCTCCAG  
 ACCGAGGACAGCTGCCCATGCCCGAGCTCCTGGCACTACCTGAGCCGGAGACCCAG  
 GACTGGCGGCCCATGCCCGAGTAGTTCTAGGGGGCGTGCTGCCAGTGGACTGGC  
 CTGCAGGTGAGCACTGCCCGGCTCTGGCTGGTCTGCTCTGCTGCCAGCAGGGAG  
 AGGGGCCATCTGATGCTTCCCTGGGAATCTAAACTGGGAATGCCGAGGAGGAAGGGGCTC  
 TGTGCACTGCAGGCCACGTCAAGGAGAGCCAGCGGTGCCTGTCGGGGAGGGTCAAGGTGC  
 TCCGTGAAGAGCATGGCAAGTTGTCTGACACTGGTGGATTCTGGTCCCTGTGGACCT  
 TGTGCATGCATGGCCTCTCTGAGCCTGGTTCTCAGCAGTGAGATGCTCAGAATAACTG  
 CTGTCTCCCATGATGGTGTGGTACAGCGAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGG  
 GGTGTTGCTGAGGGCTTGTGCCAGAGCCAGCCAGAGAGCAGGTGCAGGTGTCACTCCC  
 GAGTTCAAGGCTCTGCACGGCATGGAGTGGGAACCCCACCAAGCTGCTACAGGACCTGGGA  
 TTGCCTGGACTCCCACCTTCTATCAATTCTCATGGTAGTCAAACACTGCAGACTCTCAAAC  
 TTGCTCATT

## **FIGURE 66**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842
><subunit 1 of 1, 331 aa, 1 stop
><MW: 35932, pI: 8.45, NX(S/T): 1
MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARRG
GNIILACRDMEKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIEEEERVDILINN
AGVMRCPHWTTEDGFEMQFGVNHLGHFLLTNLLLKLKASAPSRIINLSSLAHVAGHIDFDD
LNWQTRKYNTKAAYCQSCLAIQLFTKELSRRLQGSGVTVNALHPGVARTELGRHTGIHGSTF
SSTTLGPIFWLLVKSPELAAQPSTYLAVALADVSGKYFDGLKQKAPAPEAEDEEVARRLW
AESARLVGLEAPSvreQPLPR
```

**Signal peptide:**

amino acids 1-17

## **FIGURE 67**

GAAGTTCGCGAGCGCTGGC**ATG**TGGCCTGGGGCGCGCTGGCGGCCTGCTGGCGGTGCTG  
 GCGCTCGGGACAGGAGACCCAGAAAGGCTGCGGCTCGGGCGACACGTTCTCGGCCTGAC  
 CAGCGTGGCGCGCCCTGGCGCCCGAGCGCCGGCTGCTGGGGCTGCTGAGGCCTGACCTGC  
 GCGGGGAGGAGGCGCGGCTGCGGGACCTGACTAGATTCTACGACAAGGTACTTCATGCAT  
 GAGGATTCAACAAACCCCTGTGGCTAACCCCTGCTGCTTACTCTCATCAAACGCTGCA  
 GTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTGTAAGG  
 ATGGCTATGAGAAGGTGGAGCAAGACCTCCAGCCTTGAGGACCTTGAGGGAGCAGCAAGG  
 GCCCTGATGCGGCTGCAGGACGTGTACATGCTCAATGTGAAAGGCCTGGCCGAGGTGTCTT  
 TCAGAGAGTCAGTGGCTCTGCCATCACTGACCTGTACAGCCCCAACGGCTTTCTCTCA  
 CAGGGGATGACTGCTCCAAGTTGGCAAGGTGGCTATGACATGGGGGATTATTACCATGCC  
 ATTCCATGGCTGGAGGAGGCTGTCAGTCTCTTCCGAGGATCTTACGGAGAGTGGAAAGACAGA  
 GGATGAGGCAAGTCTAGAAGATGCCCTGGATCACTTGGCTTGTCTTACAGCCCAGATAATAAGAGG  
 ATGTTCTGTGCCCCCTCAGCCTCTCTCGGGAGTTCTCTACAGCCCAGATAATAAGAGG  
 ATGGCCAGGAATGTCTGAAATATGAAAGGCTCTGGCAGAGAGCCCCAACACGTGGTAGC  
 TGAGGCTGTCACTCCAGAGGCCAATATAACCCACCTGCAGACCAGAGACACCTACGAGGGGC  
 TATGTCAGACCCCTGGGTTCCCAGCCCACCTCTACCAAGATCCCTAGCCTCTACTGTTCTAT  
 GAGACCAATTCCAACGCCAACCTGCTGCTCCAGCCATCCGGAAGGGAGGTACCCACCTGG  
 GCCCTACATTGCTCTTACCATGACTTCGTCACTGACTCAGAGGCTCAGAAAATTAGAGAAC  
 TTGCAGAACCATGGCTACAGAGGTCACTGGTGGCATCAGGGGAGAAGCAGTTACAAGTGGAG  
 TACCGCATCAGAAAAGTGCCTGGCTGAAGGACACTGTTGACCCAAAATGGTGACCCCTCAA  
 CCACCGCATTGCTGCCCTCACAGGCCTTGTATGTCCGGCTCCCTATGCAGAGTATCTGCAGG  
 TGGTGAACTATGGCATCGGAGGACACTATGAGCCTCACTTGTACGACACGTCACCAAGC  
 AGCCCCCTTACAGAACATGAAGTCAGGAAACCGAGTTGCAACATTATGATCTATGAGCTC  
 GGTGGAAGCTGGAGGAGCCACAGCCTTACATCTATGCCAACCTCAGCGTGCCTGTGGTTAGGA  
 ATGCAGCACTGTTGGTGGAACCTGCACAGGAGTGGTGAAGGGGACAGTGACACACTTCAT  
 GCTGGCTGTCTGTCTGGTGGAGATAAGTGGGTGGCCAACAAGTGGATACATGAGTATGG  
 ACAGGAATTCCGAGACCCCTGCAAGCTCCAGCCCTGAAGACT**TGA**ACTGTTGGCAGAGAGAAC  
 TGGTGGAGTCTGTGGCTTCCAGAGAACGCCAGGAGCCAAAAGCTGGGTAGGAGAGGAGAA  
 AGCAGAGCAGCCTCTGGAAAGAACGGCCTTGTCACTTGTCTGTGCCTCGCAAATCAGAGGC  
 AAGGGAGAGGTTGTTACCAAGGGACACTGAGAACATGTACATTGATCTGCCCAAGCCACGGAA  
 GTCAGAGTAGGATGCACAGTACAAAGGAGGGGGAGTGGAGGCCAGAGGGAAAGTTCTGG  
 AGTTCAAGATACTCTGTGGAACAGGACATCTCAACAGTCTCAGGTTGATCAGTGGTC  
 TTTGGCACTTGAACCTTGACCACAGGGACCAAGAACAGTGGCAATGAGGACACCTGCAGGAG  
 GGGCTAGCCTGACTCCAGAACCTTAAGACTTCTCCCCACTGCCTCTGCTGCAGCCCAAG  
 CAGGGAGTGTCCCCCTCCCAGAACATCCCAGATGAGTGGTACATTATATAAGGATTTT  
 TTTAAGTTGAAAACAACCTTCTTTCTTTGTATGATGGTTTTAACACAGTCATTAAAA  
 ATGTTATAAATCAAAA

100156410 - 121204

## **FIGURE 68**

MGPGARLAALLAVLALGTGDPERAARGDTFSALTSGVARALAPERRLLGLLRRYLRGEEARL  
RDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVVHSLEASENIRALKDGYEKVE  
QDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRVTGSAITDLYSPKRLFSLTGDDCFQ  
VGKVAYDMGDYYHAIPWLEEAVSLFRGSYGEWKTEDEASLEDALDHLAGFAYFRAGNVSCALS  
LSREFLLYSPDNKRMARNVLKYERLLAESPNHVVAEAVIQRPNIPHQLQTRDTYEGLCQTLGS  
QPTLYQIPSLYCSYETNSNAYLLLQPIRKEVILLEPYIALYHDFVSDSEAQKIRELAEPWLQ  
RSVVVASGEKQLQVEYRISKSAWLKDTVDPKLVTLNHRIAALTGLDVRPPYAELYQVVNYGIG  
GHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLSSVEAGGATAFIYANLSVPVVRNAALFWW  
NLHRSGEGDSDLHAGCPVLVGDKWVANKWIHEYGQEFRRPCSSSPED

**Signal peptide:**

amino acids 1-19

## **FIGURE 69**

GAGATAGGGAGTCTGGGTTAAGTCCTGCTCCATCTCAGGAGCCCCGTGCTCCCACCCCTAG  
 GAAGGCCACCAGACTCCACGGTGTGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGCC  
 ACGAGCGCTGGCTGAGGGACCGAGCCGGAGAGCCCCGGAGCCCCCGTAACCCGCGCGGGAG  
 CGCCCAGGATGCCGCGCGGGACTCGGAGCAGGTGCGCTACTGCGCGCCTTCTCCTACCTC  
 TGGCTCAAGTTTCACTTATCATCTATTCCACCGTGTCTGGCTGATTGGGCCCTGGTCT  
 GTCTGTGGCATCTATGCAGAGGTTGAGCGGCAGAAATATAAAACCTTGAAAGTGCCTTCC  
 TGGCTCCAGCCATCATCCTCATCCTGGCGTGTGTCATGTTATGGTCTCCTCATTGGT  
 GTGCTGGCGTCCCTCCGTGACAACCTGTACCTTCTCCAAGCATTGTCATGTACATCCTGGGAT  
 CTGCCTCATCATGGAGCTCATTGGTGGCGTGGTGGCCTTGACCTTCCGGAACCAGACCATTG  
 ACTTCCTGAACGACAACATTCGAACAGAGGAATTGAGAACTACTATGATGATCTGGACTTC  
 AACATCATGGACTTTGTTCAGAAAAAGTTCAAGTGCTGTGGCGGGGAGGACTACCGAGATTG  
 GAGCAAGAACATCAGTACACGACTGCAGTGCCCCCTGGACCCCTGGCCTGTGGGTGCCCTACA  
 CCTGCTGCATCAGGAACACGACAGAACAGTTGTCACACACCATGTGTGGCTACAAA  
 AACATCGAC  
 AAGGAGCGTTCAGTGTGCAGGATGTCATCTACGTGCGGGCTGCACCAACGCCGTGATCAT  
 CTGGTTCATGGACAACCATACCATGGCGTGCATCCTCCTGGCATTGCTTCCCCAGT  
 TCCTGGGGGTGCTGCTGACGCTGTCATCACCCGGTGGAGGACATCATGGAGCAC  
 TCTGTCACTGATGGCCTCTGGGCCCGGTGCCAACGCCAGCGTGGAGGCGGCAGGCACGGG  
 ATGCTGCTTGTGCTACCCAAATTAGGGGCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTC  
 TGGGATAGCACCTCTCAGTCAACATCGTGGGCTGGACAGGGCTGCCCTCTGCCACA  
 CTCAGTACTGACCAAAGCCAGGGCTGTGTGCCTGTGTAGGTCCCACGCCCTGCCTC  
 CCCAGGGAGCAGAGCCTGGCCTCCCTAACAGAGGCTTCCCCGAGGCAGCTCTGGAATCTGT  
 GCCCACCTGGGCCTGGGAACAAGGCCCTCCTTCTCCAGGCCTGGCTACAGGGAGGGA  
 GAGCCTGAGGCTCTGCTCAGGCCATTTCATCTGGCAGTGCCTGGCGGTGGTATTCAA  
 GGCAGTTTGTAGCACCTGTAATTGGGAGAGGGAGTGTGCCCTCGGGCAGGAGGGAAGG  
 GCATCTGGGAAGGGCAGGAGGGAAGAGACTGTCCATGCAGCCACGCCATGCCAGGTTGGC  
 CTCTCTCAGCCTCCAGGTGCCTTGAGCCCTTGTCAAGGGCGGCTGCTCCTTGAGCCTA  
 GTTTTTTACGTGATTTGTAACATTCACTTTGTACAGATAACAGGAGTTCTGAC  
 TAATCAAAGCTGGTATTCGGCATGTCTATTCTGCCCTCCCCAACCAGTTGTTAA  
 TCAAACAATAAAACATGTTGTTGTTAAAAAAA

## FIGURE 70

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863
><subunit 1 of 1, 294 aa, 1 stop
><MW: 33211, pI: 5.35, NX(S/T): 3
MPRGDSEQVRYCARFSYWLKFSLIIYSTVFWLIGALVLSVGIYAEVERQKYKTLESAFLAP
AIILILLGVVMFMVSFIGVLASLRDNLYLLQAFMYILGICLIMELIGGVVALTFRNQTIDFL
NDNIIRGIENYYDDLDFKNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPGPLACGVPYTCC
IRNTTEVVNTMCGYKTIDKERFSVQDVYVRGCTNAVIIWFMDNYTIMACILLGILLPQFLG
VLLTLLYITRVEDIIMEHSVTDGLLGPGAKPSVEAAGTGCCLCYPN
```

**Signal peptide:**

amino acids 1-44

**Transmembrane domains:**

amino acids 22-42, 57-85, 93-116, 230-257

## **FIGURE 71**

GAGGAGCGGGCCGAGGACTCCAGCGTCCCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGA  
 CACCTGGGAAG**ATGGCCGGCCCGTGGACCTTCACCCTCTGTGGTTGCTGGCAGCCACC**  
 TTGATCCAAGCCACCCTCAGTCCCCTGCAGTTCTCATCCTCGGCCAAAAGTCATCAAAGA  
 AAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGC  
 TCAGTGCCATGCCGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGCAGCCTGGTAAACACC  
 GTCCTGAAGCACATCATCTGGCTGAAGGTCACTCACAGCTAACATCCTCCAGCTGCAGGTGAA  
 GCCCTCGGCCAATGACCAGGAGCTGCTAGTCAGATCCCCCTGGACATGGTGGCTGGATTCA  
 ACACGCCCTGGTCAAGACCATCGTGGAGTTCCACATGACGACTGAGGCCAAGCCACCATC  
 CGCATGGACACCAGTGCAAGTGGCCCCACCCGCTGGTCTCAGTGACTGTGCCACCAGCCA  
 TGGGAGCCTGCGCATCCAAGTGTGTTGACCTCTGGTGAACGCCCTAGCTAACGC  
 AGGTCACTGAACCTCCTAGTGCCATCCCTGCCAATCTAGTGAAAACCAGCTGTGTCCCCTG  
 ATCGAGGCTTCCTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCATTTC  
 CCTCAGCATTGACCGTCTGGAGTTGACCTCTGTATCCTGCCATCAAGGGTGACACCATTC  
 AGCTCTACCTGGGGCCAAGTTGTTGGACTCACAGGGAAAGGTGACCAAGTGGTTCAATAAC  
 TCTGCAGCTTCCTGACAATGCCAACCTGGACAACATCCGTTAGCCTCATCGTGAGTCA  
 GGACGTGGTGAAGCTGCAGTGGCTGCTGTGCTCTCCAGAAGAATTGATGGTCTGTTGG  
 ACTCTGTGCTTCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATTGAGATCCGCTGATCAATGAAAAG  
 GCTGCAGATAAGCTGGATCTACCCAGATCGTAAGATCCTAACTCAGGACACTCCGAGTT  
 TTTTATAGACCAAGGCCATGCCAAGGTGGCCAAGTGTGCTGGAAAGTGGTCCCTCCA  
 GTGAAGCCCTCCGCCCTTGTTCACCCCTGGCATCGAAGCCAGCTCGGAAGCTCAGTTTAC  
 ACCAAAGGTGACCAACTTATACTCAACTGAAATAACATCAGCTCTGATCGGATCCAGCTGAT  
 GAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCC  
 ACTCCATCCTGCTGCCGAACCAGAAATGGCAAATTAAAGATCTGGGTCCCAGTGTGATTGGT  
 AAGGCCTTGGGATTGAGGCAGCTGAGTCCTCACTGACCAAGGATGCCCTGTGCTTACTCC  
 AGCCTCCTTGTGGAAACCCAGCTCCTGTCTCCAG**TGAAGACTTGGATGGCAGCCATCAG**  
 GGAAGGCTGGTCCCAGCTGGAGTATGGGTGTGAGCTATAGACCATCCCTCTGCAAT  
 CAATAAACACTTGCCTGTGAAAAA

**FIGURE 72**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881
><subunit 1 of 1, 484 aa, 1 stop
><MW: 52468, pI: 7.14, NX(S/T): 3
MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILQQLPLSAM
REKPAGGI PVLGSLVNTVLKHI IWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPL
VKTIVEFHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMN
LLVPSLPNLVKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDTIQLYL
GAKLLDSQGKVTKWFNNSAASLTMP LDNIPFSLIVSQDVVKAAVAAVLSPEEFMVLLDSVL
PESAHRLKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSeAL
RPLFTLGIEASSEAQFYTKGDQLI LNLNNI SDRQLMNSGIGWFQPDVLKNIITEIIHSIL
LPNQNGKLRSGVPVSLVKALGFEEAESSLTKDALVLTPASLWKPSSPVSQ
```

**Important features of the protein:****Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 48-51, 264-267, 401-404

**Glycosaminoglycan attachment site.**

amino acids 412-415

**LBP / BPI / CETP family proteins.**

amino acids 407-457

## **FIGURE 73**

GAGCGAAC**ATG**GCAGCGCGTGGCGTTGGTGTCTCTGTGACCATGGTGGTGGCGCTG  
 CTCATCGTTGCGACGTTCCCTCAGCCTCTGCCAAAGAAAGAAGGAGATGGTGTATCTGA  
 AAAGGTTAGTCAGCTGATGGAATGGACTAACAAAAGACCTGTAATAAGAATGAATGGAGACA  
 AGTTCGTCGCCTTGTGAAAGCCCCACCGAGAAATTACTCCGTTATCGTCATGTTCACTGCT  
 CTCCAAGTCGATAGACAGTGTGTCGTTGCAAGCAAGCTGATGAAGAATTCCAGATCCTGGC  
 AAACTCCTGGCGATACTCCAGTGCATTACCAACAGGATATTTTGCCATGGTGGATTTG  
 ATGAAGGCTCTGATGTATTCAGATGCTAAACATGAATTCACTGCTCAAATTTCATCAACTTT  
 CCTGCAAAAGGGAAACCCAAACGGGGTGATACATATGAGTTACAGGTGCGGGGTTTCAGC  
 TGAGCAGATTGCCCGGTGGATCGCCGACAGAACTGATGTCATATTAGAGTGATTAGACCCC  
 CAAATTATGCTGGTCCCTTATGTTGGGATTGCTTTGGCTGTTATTGGTGGACTTGTGTAT  
 CTTCGAAGAAGTAATATGAAATTCTCTTTAATAAAACTGGATGGCTTTGAGCTTGTG  
 TTTTGTGCTTGCTATGACATCTGGTCAAATGTGGAACCATAAGAGGACCACCATATGCC  
 ATAAGAATCCCCACACGGGACATGTGAATTATATCCATGAAAGCAGTCAAGCCCAGTTGTA  
 GCTGAAACACACATTGTTCTGTTAATGGTGGAGTTACCTTAGGAATGGTGTGGCTGGTATTG  
 TGAAGCTGCTACCTCTGACATGGATATTGAAAGCGAAAGATAATGTGTGTGGCTGGTATTG  
 GACTTGTGTATTATTCTCAGTTGGATGCTCTATTAGATCTAAATATCATGGCTAC  
 CCATACAGCTTCTGATGAGT**TAAA**AGGTCCCAGAGATATAGACACTGGAGTACTGGAA  
 ATTGAAAAACGAAATCGTGTGTTGAAAAGAAGAATGCAACTGTATATTGTATTAC  
 CTCTTTTTCAAGTGAATTAAAGTTAATCATTAAACAAAGAAGATGTGTAGTGCCTTA  
 ACAAGCAATCCTCTGTCAAATCTGAGGTATTGAAAATAATTATCCTCTTAACCTCTCTT  
 CCCAGTGAACTTATGGAACATTAAATTAGTACAATTAAAGTATATTATAAAATTGAAAA  
 CTACTACTTGTGTTAGTTAGAACAAAGCTAAAACACTTTAGTTAACCTGGTCATCTGAT  
 TTTATATTGCCTTATCCAAAGATGGGAAAGTAAGTCCCTGACCAGGTGTTCCCACATATGCC  
 TGTTACAGATAACTACATTAGGAATTCTAGCTTCTCATCTTGTGTGGATGTGTAT  
 ACTTACGCATCTTCTTTGAGTAGAGAAATTATGTGTGTATGTGGCTTCTGAAATG  
 GAACACCATTCTCAGAGCACACGTCTAGCCCTCAGCAAGACAGTTGTTCTCTCCT  
 GCATATTCTACTGCGCTCCAGCCTGAGTGTAGAGACTCTGTCATAAAAAAGTA  
 TCTCTAAATAACAGGATTATAATTCTGCTTGAGTATGGTGTAACTACCTGTATTAGAAA  
 GATTTCAGATTCATTCCATCTCCTTAGTTCTTAAGGTGACCCATCTGTGATAAAAATA  
 TAGCTTAGTGCTAAAATCAGTGTAACTTACATGGCTAAAATGTTCTACAAATTAGAGT  
 TTGTCACTTATTCCATTGTACCTAAGAGAAAATAGGCTCAGTTAGAAAAGGACTCCCTGG  
 CCAGGGCAGTGACTTACGCCTGTAATCTCAGCACTTGGGAGGCCAAGGCAGGCAGATCAC  
 GAGGTGAGGAGTTGAGACCATCCTGGCAACATGGTGAACACCCGTCTACTAAAATA  
 AAAAATTAGCTGGGTGTGGTGGCAGGAGCCTGTAATCCCAGCTACACAGGAGGCTGAGGCAC  
 GAGAATCACTGAACTCAGGAGATGGAGGTTCACTGAGCCGAGATCACGCCACTGCACTCC  
 AGCCTGGCAACAGAGCGAGACTCCATCTCAAAAAAAAAAA

## **FIGURE 74**

MAARWRFWCVSVTMVALLIVCDVPSASAQRKKEMVLSEKVSQLMETNKRPVIRMNGDKFR  
RLVKAPPRNYSVIVMFALQLHRQCVVCKQADEFQILANSWRYSSAFTNRIFFAMVDFDEG  
SDVFQMLNMNSAPTFINFPAKGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY  
AGPLMLGLLLAVIGGLVYLRRSNMEFLFNKTGWAFAAACFVLAMTSQMWNHIRGPPYAHKN  
PHTGHVNYIHGSQAQFVAETHIVLLFNGGVTLMVLLCEAATSDMDIGKRKIMCVAGIGLV  
VLFFSWMLSIFRSKYHGYPSFLMS

**Signal peptide:**

amino acids 1-29

**Transmembrane domains:**

amino acids 183-205, 217-237, 217-287, 301-321



## **FIGURE 76**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885
<subunit 1 of 1, 536 aa, 1 stop
<MW: 61450, pI: 9.17, NX(S/T): 7
MLLLWVSVVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDSFDGRLTFHPGSQVVKLPFINF
MKTRGTSFLNAYTNSPICCPsRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQ
KFGKLDYTSGHHSISNRVEAWTRDVAFLRQEGRPMVNLI RNRTKVRVMERDWQNTDKAVNW
LRKEAINYTEPFVIYLGLNLPHYPSPSSGENFGSSTFHTSLYWLEKVSHDAIKIPKWSPLS
EMHPVDYYSSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQDLLQKTIVIY
SSDHGELAMEHRQFYKMSMYEASAHVPLLMMGPGIKAGLQVSNVVSLVDIYPTMLDIAGIPL
PQNLSGYSLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYSDGAS
ILPQLFDLSSDPDELNVAVKFPEITYSLDQKLHSIIINYPKVSASVHQYNKEQFIKWQSIG
QNYSNVIANLRWHQDWQKEPRKYENAI DQWLKTHMN PRAV
```

**Important features:**

**Signal peptide:**

amino acids 1-15

**N-glycosylation sites.**

amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,  
498-501

**Sulfatases proteins:**

amino acids 286-315, 359-369, 78-97

## FIGURE 77

GAGAGAAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG  
AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCATG  
GCCTCTTGGCCTCCAACTTGTGGCTACATCCTAGGCCTCTGGGCTTGGGACACT  
GGTTGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTCGGTGCCAGCATTGTGACAG  
CAGTTGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCAG  
TGTGACATCTATAGCACCCCTCTGGGCTGCCGCTGACATCCAGGCTGCCAGGCCATGAT  
GGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGCATGAGATGCA  
CAGTCTTCTGCCAGGAATCCCGAGCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTC  
ATCCTGGAGGCCTCTGGATTCTTCCTGTTGCCTGGAATCTCATGGGATCCTACGGGA  
CTTCTACTCACCACTGGTGCCTGACAGCATGAAATTGAGATTGGAGAGGCTCTTACTTGG  
GCATTATTTCTCCCTGTTCTCCCTGATAAGCTGGAATCATCCTCTGCTTTCTGCTCATCC  
CAGAGAAATCGCTCCAACTAACGATGCCAACCTTGTGCCACAAGGAGCTC  
TCCAAGGCCTGGTCAACCTCCAAAGTCAAGAGTGAAGTCAATTCTACAGCCTGACAGGGT  
ATGTGTGAAGAACCCAGGGCCAGAGCTGGGGGTGGCTGGTCTGTGAAAAACAGTGGACAG  
CACCCCGAGGCCACAGGTGAGGGACACTACCACTGGATCGTGTAGAAGGTGCTGCTGAGG  
ATAGACTGACTTGGCATTGGATTGAGCAAAGGCAGAAATGGGGCTAGTGTAAACAGCATG  
CAGGTTGAATTGCCAAGGATGCTGCCATGCCAGCCTTCTGTTCTCACCTGCTGCTGCTC  
CCCTGCCCTAACGCCCCAACCTCAACTTGAAACCCATTCCCTAACGCCAGGACTCAGAGG  
ATCCCTTGTCCCTGTGTTACCTGGACTCCATCCCCAACCCACTAACATCACATCCACTG  
ACTGACCCCTGTGATCAAAGACCCCTCTCTGGCTGAGGTTGGCTTAGCTCATTGCTGG  
GGATGGGAAGGAGAAGCAGTGGCTTGTGGCATTGCTCTAACCTACTTCTCAAGCTTCCC  
TCCAAAGAAACTGATTGCCCTGGAACCTCCATCCACTCTGTTATGACTCCACAGTGTCC  
AGACTAATTGTGCATGAACTGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAG  
GATGCAGGATGGGAGGACAGGAAGGCAGCCTGGACATTAAAAAAATA

## **FIGURE 78**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886
><subunit 1 of 1, 230 aa, 1 stop
><MW: 24549, pI: 8.56, NX(S/T): 1
MASLGLQLVGYILGLLGLGTIVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGIT
QCDIYSTLLGLPADIQAAQAMMVTSSAISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVF
FILGGLLGFIPVAWNLHGILRDFYSPLVPSMKEIGEALYLGISSLFSLIAGIILCFSCS
SQQRNRSNYYDAYQAQPLATRSSPRPGQPPKVKEFNSYSLTGYV
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 82-102, 117-140, 163-182

**N-glycosylation site.**

amino acids 190-193

**PMP-22 / EMP / MP20 family proteins.**

amino acids 46-59

**FIGURE 79**

GCAC TGCT GCT GTCCC ATCAG CTGCT CTGA AGCT CC **ATGGT** GCC CAGA ATCT CGCT CCT GC  
TTAT GTGT CAGT CTGT CTCC TCT CTT GTGT CCA AGGG AAGT CATCG CTCC GCT GGCT CAG  
AACCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTGGAGCAG  
TGCT GTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCAATGTGGTCCCCCTGCAC  
CTTCTGGCCCTGCTT GAGCTCTGCTGTGATT CTTGGCCTCACAAACGATT TTGTTG  
TGAAGCTGAAGGTT CAGGGTGTGA ATT CCCAGT GCCACTCATCTCCATCTCCAGTAAATGT  
GAAAGCAGAAGACGTTTCCC **TGA** GAAGACATAGAAAGAAAATCAACTTCACTAAGGCATC  
TCAGAAACATAGGCTAAGGTAATATGTGTACCA GTAGAGAAGCCTGAGGAATTACAAAATG  
ATGCAGCTCCAAGCCATTGTATGGCCATGTGGGAGACTGATGGGACATGGAGAATGACAGT  
AGATTATCAGGAAATAATAAGTGGTTTCCAATGTACACACCTGTAAAA

## **FIGURE 80**

MVPRIFAPAYVSVC~~LLL~~CPREVIAPAGSEPWLQPA~~P~~R~~C~~GDKIYNPLEQCCYND~~A~~I~~V~~SLSE  
TRQCGPPCTFWPCFELCCLDSFG~~L~~TNDFVVKLKVQGVNSQCHSSPISSKCESRRRFP

**Signal peptide:**

amino acids 1-25

**FIGURE 81**

CTCCACTGCAACCACCCAGAGCC**ATG**GCTCCCCGAGGCTGCATCGTAGCTGTCTTGCATT  
TTCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCT  
GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCCCTGCAGCACTGTT  
GCTATGATGATGCCGTCGTGCCCTGGCCAGGACCCAGACGTGTGGAAACTGCACCTTCAGA  
GTCTGCTTGAGCAGTGCTGCCCTGGACCTTCATGGTGAAGCTGATAAACCAGAACTGCGA  
CTCAGCCGGACCTCGGATGACAGGCTTGTGCGAGTCAGC**TAA**TGGAACATCAGGGAA  
CGATGACTCCTGGATTCTCCTCTGGTGGCCTGGAGAAAGAGGCTGGTGTACCTGAGA  
TCTGGGATGCTGAGTGGCTGTTGGGGCCAGAGAAACACACACTCAACTGCCACTTCATT  
CTGTGACCTGTCTGAGGCCACCCCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCTCTAG  
AATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGCCAGGGACTCTGAACCCTCCTGAT  
GACCCCTATGCCAACATCAACCCGGCACCAACCCAAGGCTGGCTGGGAACCCTCACCCCT  
TCTGTGAGATTTCCATCATCTCAAGTTCTCTTCTATCCAGGAGCAAAGCACAGGATCATAA  
TAAATTATGTACTTATAAATGAAAA

## **FIGURE 82**

MAPRGCIVAVFAIFCISRLLC SHGAPVAPMTPYLM CQPHKRCGDKFYDPLQHCCYDDAVVP  
LARTQTCGNCTFRVCFEQCCPWTFMVKLINQNCD SARTSDDR LCRSVS

**Signal peptide:**

amino acids 1-24

## **FIGURE 83**

GGGGGCGGGTGCCTGGAGCACGGCGTGGGCCGCCGCAGCGCTACTCGCTCGCACTCAG  
 TCGCGGGAGGCTCCCCGCGCCGGCGTCCCCGGCTCCCCGGCACCAGAAGTTCCCTCT  
 GCGCGTCCGACGGCGACATGGGCGTCCCCACGGCCCTGGAGGCCAGCTGGCGTGGGA  
 TCCCTGCTCTCGCTCTTCCTGGCTGCGTCCCTAGGTCCGGTGGCAGCCTCAAGGTGCG  
 CACGCCGTATTCCCTGTATGTCTGTCCCAGGGCAGAACGTACCCCTACCTGCAGGCTCT  
 TGGGCCCTGTGGACAAAGGCACGATGTGACCTCTACAAGACGTGGTACCGCAGCTCGAGG  
 GGCGAGGTGCAGACCTGCTCAGAGGCCGGCCCATCCGCAACCTCACGTTCCAGGACCTTCA  
 CCTGCACCAGGAGGCCACCAGGCTGCCAACACCAGGCCACGACCTGGCTCAGGCCACGGC  
 TGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATACCATGCGAACCTGACCTGCTG  
 GATAGCGGCCTCTACTGCTGCCTGGTGGAGATCAGGCACCACACTGGAGCACAGGGT  
 CCATGGTGCCATGGAGCTGCAGGTGCAGACAGGCAAAGATGCACCATCCAACATGTGTGGTGT  
 ACCCATCCTCCTCCCAGGATAGTGAAAACATCACGGCTGCAGCCCTGGCTACGGGTGCCTGC  
 ATCGTAGGAATCCTCTGCCTCCCCCTATCCTGCTCCTGGTCTACAAGCAAAGGCAGGCAGC  
 CTCCAACCGCCGTGCCAGGAGCTGGTGCAGGATGGACAGCAACATTCAAGGGATTGAAAACC  
 CCGGCTTGAAGCCTCACCACCTGCCAGGGATAACCGAGGCCAAAGTCAGGCACCCCTG  
 TCCTATGTGGCCCAGCGGCAGCCTCTGAGTCTGGCGGCATCTGCTTGGAGGCCAGCAC  
 CCCCCCTGTCTCCTCCAGGCCCCGGAGACGTCTTCTCCATCCCTGGACCCCTGTCCCTGACT  
 CTCCAAACTTGAGGTACTAGCCCAGCTGGGGACAGTGGCTGTTGTGGCTGGGTCTGG  
 GGCAGGTGCATTGAGCCAGGGCTGGCTCTGTGAGTGGCCTCCTGGCCTGGCCCTGGTTC  
 CCTCCCTCCTGCTCTGGCTCAGATACTGTGACATCCCAGAACGCCAGCCCTCAACCCCTC  
 TGGATGCTACATGGGATGCTGGACGGCTCAGCCCTGTTCCAAGGATTTGGGTGCTGAG  
 ATTCTCCCCTAGAGACCTGAAATTCAACCAGCTACAGATGCCAAATGACTTACATCTTAAGAA  
 GTCTCAGAACGTCCAGCCCTCAGCAGCTCTGTTCTGAGACATGAGCCTGGATGTGGCA  
 GCATCAGTGGACAAGATGGACACTGGCCACCCCTCCAGGCACCAGACACAGGGCACGGT  
 GAGAGACTTCTCCCCGTGGCCGCTGGCTCCCCGTTGGCCGAGGCTGCTCTGTGTC  
 AGACTTCCCTTTGTACCACAGTGGCTCTGGGCCAGGCCTGCCACTGCCATGCC  
 ACCTTCCCCAGCTGCCTCCTACCAGCAGTTCTGAAAGATCTGTCAACAGGTTAAGTCAAT  
 CTGGGCTTCCACTGCCTGCATTCCAGTCCCCAGAGCTGGTGGTCCGAAACGGGAAGTAC  
 ATATTGGGCATGGTGGCCTCCGTGAGCAAATGGTGTCTTGGCAATCTGAGGCCAGGACAG  
 ATGTTGCCCAACCCACTGGAGATGGTGTGAGGGAGGTGGTGGGCCCTCTGGGAAGGTGA  
 GTGGAGAGGGCACCTGCCCTCCCCATCCCTACTCCACTGCTCAGCGCGGGCC  
 ATTGCAAGGGTGCCACACAATGTCTGTCCACCTGGACACTTCTGAGTATGAAGCGGGAT  
 GCTATTAAAAACTACATGGGAAAAAAAAAAAAAAAAAAAAAAAAGA

**FIGURE 84**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897
><subunit 1 of 1, 311 aa, 1 stop
><MW: 33908, pI: 6.87, NX(S/T): 6
MGVPTALEAGSWRWGSILLFALFLAASLGPVAAFKVATPYSLYVCPEGQNVTLTCRLLGPVDK
GHDVTFYKTWYRSSRGEVQTCERRPIRNLTFQDLHLHHGGHQAANTSHDLAQRHGLEASAD
HHGNFSITMRNLTLLDGLYCCLVVEIRHHSEHRVHGAMELQVQTGKDAPSNCVVPSSSQ
DSENITAAALATGACIVGILCPLLLLVLVYKQRQAASNRAQELVRMDSNIQGIENPGFEAS
PPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSPPPGDVFFPSLDPPDSPNFEVI
```

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 190-216

## **FIGURE 85**

CCCACGCGTCCCGCCTCTCCCTCTGCTGGACCTTCCTCGTCTCCATCTCTCCCTCCT  
 TTCCCCCGTTCTCTTCCACCTTCTCTTCCCACCTAGACCTCCCTCCTGCCCTCC  
 TTTCTGCCAACCGCTGTTCTGGCCCTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGG  
 GGTCTGTGGGTTGATCTGTGGCCCTGTGCCTCCGTGTCCTTCGTCTCCCTCCTCCGA  
 CTCCGCTCCCGGACCAGCGGCCTGACCTGGGGAAAGGATGGTTCCCGAGGTGAGGGTCCTC  
 TCCTCCTTGCTGGACTCGCGCTGCTCTGGTTCCCCCTGGACTCCCACGCTCGAGCCCGCCC  
 AGACATGTTCTGCCTTTCCATGGGAAGAGATACTCCCCCGCGAGAGCTGGCACCCCTACT  
 TGGAGCCACAAGGCCTGATGTAUTGCCTGCGCTGTACCTGCTCAGAGGGCGCCATGTGAGT  
 TGTTACCGCCTCCACTGTCCGCCTGTCCACTGCCCGGAGCCTGTGACGGAGCCACAGCAATG  
 CTGTCCAAGTGTGTGGAACCTCACACTCCCTCTGGACTCCGGGCCCCACCAAAGTCCTGCC  
 AGCACAACGGGACCATGTACCAACACGGAGAGATCTTCAGTGCCTCATGAGCTGTTCCCCCTCC  
 CGCCTGCCAACCAGTGTGTCCCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCCTCAC  
 AACCTGCCCGAACCAAGGCTGCCAGCACCCCTCCACTGCCAGACTCCTGCTGCCAACGCT  
 GCAAAGATGAGGCAAGTGTGAGCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGTG  
 AGACATCCTCAGGATCCATGTTCCAGTGTGCTGGAGAAAGAGAGGGCCGGCACCCAGC  
 CCCCACGGCCTCAGGCCCTCTGAGCTTCATCCCTGCCACTTCAGACCCAAGGGAGCAG  
 GCAGCACAACTGTCAAGATCGTCCCTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGGCGGG  
 AAGACGTACTCCCACGGGAGGTGTGGCACCCGGCCTCCGTGCCTCGGCCCTTGCCCTG  
 CATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGT  
 ACCCCTGCCGTACCCCGAGAAAGTGGCTGGGAAGTGTGCTGCAAGATTGCCAGAGGACAAA  
 GCAGACCCCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCAAGGCACCGGGCGGGTCT  
 CGTCCACACATCGGTATCCCCAAGCCAGACAACCTGCGTCGCTTGCCCTGGAACACGAGG  
 CCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAAACTGAGGCTCAG  
 AGAGGTGAAGTACCTGGCCAAGGCCACACAGCCAGAATCTTCCACTGACTCAGATCAAGA  
 AAGTCAGGAAGCAAGACTCCAGAAAGAGGCACAGCACTCCGACTGCTCGCTGGCCCCAC  
 GAAGGTCACTGGAACGTCTTCCTAGGCCAGACCCCTGGAGCTGAAGGTACGGCCAGTCCAGA  
 CAAAGTGACCAAGACATAACAAAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTGTT  
 ATTATATATTATAAAATAAGAAGTTGCATTACCCCTCAAAAAAAAAAAAAAAA

**FIGURE 86**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902  
><subunit 1 of 1, 451 aa, 1 stop  
><MW: 49675, pI: 7.15, NX(S/T): 1  
MVPEVRVLSSLLGLALLWFPLDSHARARPDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRCT  
CSEGAHVSCYRLHCPPVHCPQPVTEPQQCCPKCVEPHTPSGLRAPPKSCQHNGTMYQHGEIF  
SAHELFPSRLPNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEED  
SVQSLHGVRHPQDPCSSDAGRKRGPGT PAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKH  
KKACVHGGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPTEYPCRHPEKVAGKC  
CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKLV  
KDEETEAQRGEVPGPRPHSQNLPLSDQESQEARNPERGTALPTARWPPRRSLERLPSPDPG  
AEGHGQSRQSDQDITKT

**Signal peptide:**

amino acids 1-25

**FIGURE 87**

CTAGCCTGCGCCAAGGGTAGTGAGACCGCGCGGCAACAGCTTGC GGCTGC GGGGAGCTCCC  
GTGGCGCTCCGCTGGCTGTGCAGGC GGCCATGGATT CCTGC GGAAAATGCTGATCTCAGT  
CGCAATGCTGGCGCAGGGCTGGCGTGGCTACCGCCTCGTTATCGTACCCGGAG  
AGCGGCGGAAGCAGGAAATGCTAAAGGAGATGCCACTGCAGGACCCAAAGGAGCAGGGAGGAG  
GCGGCCAGGACCCAGCAGCTATTGCTGCCACTCTGCAGGAGGCAGCGACCACGCAGGAGAA  
CGTGGCCTGGAGGAAGAACTGGATGGTGGCGCGAAGGC GGCGCAGCGGGAGGT CACCGT  
GAGACCGGACTTGCCTCCGTGGCGCCGGACCTTGGCTTGGCGCAGGAATCCGAGGCAGCC  
TTTCTCCTCGTGGGCCAGCGGAGAGTCGGACCGAGATAACCATGCCAGGACTCTCCGGG  
TCCTGTGAGCTGCCGTGGGTGAGCACGTTCCCCAACCCCTGGACTGACTGCTTAAGGT  
CCGCAAGGCGGGCCAGGGCGAGACGCGAGTCGGATGTGGTGAAGTGAACAAAAAAACCAATAAAA  
TCATGTTCCCTCAA  
AAAAAAAAAAA

## **FIGURE 88**

MDSLRKMLISVAMLGAGAGVGYALLVIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLA  
TLQEATTQENVAWRKNWMVGEGGASGRSP

**Signal peptide:**

amino acids 1-18

**FIGURE 89**

CAGGAGAGAAGGCACGCCCAACCGCCTCCAAAGCTAACCTCGGGCTTGAGGGGAAGA  
 GGCTGACTGTACGTTCTTACTCTGGCACACTCTCCAGGCTGCC**TG**GGGCCAGCACC  
 CCTCTCCTCATCTTGTCTTGTATGGTCGGGACCCCTCCAAGGACAGCAGCACCACT  
 TGTGGAGTACATGGAACGCCGACTAGCTGCTTAGAGGAACGGCTGGCCAGTGCAGGACC  
 AGAGTAGTCGGCATGCTGCTGAGCTGCGGGACTTCAAGAACAGATGCTGCCACTGCTGGAG  
 GTGGCAGAGAAGGAGCGGGAGGCACTCAGAACTGAGGCCGACACCATCTCGGGAGAGTGG  
 TCGTCTGGAGCGGGAGGTAGACTATCTGGAGACCCAGAACCCAGCTCTGCCCTGTAGAGT  
 TTGATGAGAAGGTGACTGGAGGCCCTGGGACCAAAGGAAGGGAAAGGAATGAGAAAGTAC  
 GATATGGTGACAGACTGTGGCTACACAATCTCAAGTGAGATCAATGAAGATTCTGAAGCG  
 ATTTGGTGGCCCAGCTGGTCTATGGACCAAGGATCCACTGGGGCAAACAGAGAAGATCTACG  
 TGTTAGATGGGACACAGAACATGACACAGCCTTGTCTCCAAAGGCTGCGTGACTTCACCC  
 GCCATGGCTGCCCGGAAAGCTCCGAGTCCGGGTGCCCTCCCTGGTAGGCACAGGGCA  
 GCTGGTATATGGTGGCTTCTTATTTGCTCGGAGGCCTCCTGGAAGACACTGGTGGAGGTG  
 GTGAGATGGAGAACACTTGCAGCTAACAAATTCCACCTGGCAAACCGAACAGTGGTGGAC  
 AGCTCAGTATTCCCAGCAGAGGGCTGATCCCCCCTACGGCTGACAGCAGACACCTACAT  
 CGACCTGGTAGCTGATGAGGAAGGTCTTGGCTGTCTATGCCACCCGGAGGATGACAGGC  
 ACTTGTGTCTGCCAAGTTAGATCCACAGACACTGGACACAGAGCAGCAGTGGACACACCA  
 TGTCCCAGAGAGAACATGCTGAGGCTGCCTTGTATCTGGGACCTCTATGTCGTCTATAA  
 CACCGTCCTGCCAGTCGGGCCGCATCCAGTGCTCCTTGATGCCAGCGCACCC  
 CTGAACGGGCAGCACTCCCTATTTCCCGAGATATGGTGCCTGCCAGCCTCCGCTAT  
 AACCCCCGAGAACGCCAGCTCATGCCCTGGGATGATGGCTACCAAGATTGCTATAAGCTGGA  
 GATGAGGAAGAAAGAGGGAGGAGGTT**TGA**GGAGCTAGCCTGTTGCATCTTCACTC  
 CCATACATTATATTATATCCCCACTAAATTCTTGTCTCATTCTCAAATGTGGCCAG  
 TTGTGGCTCAAATCCTCTATATTTAGCCAATGGCAATCAAATTCTTCAGCTCCTTGTT  
 TCATACGGAACTCCAGATCCTGAGTAATCCTTAGAGCCGAAGAGTCAAAACCC  
 TTCCCTCCTGCTCCTGCCCATGTCAACAAATTCAAGGCTAACGGATGCCAG  
 GCTCTAACCTTGTATGCCGGCAGGCCAGGGAGCAGGCAGCAGTGTCTTCC  
 ACTTGGGGAGGGAGAAATAGGAGGAGACGTCCAGCAGTGTCTCTCCTC  
 TCAGTGTCTGAGGAACAGGACTTCTCACATTGTTGTATTGCAACATT  
 AGGAAAATCCACAAAAAAA  
 AAAAAAAAAAAAAAAA

## FIGURE 90

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905
<subunit 1 of 1, 406 aa, 1 stop
<MW: 46038, pI: 6.50, NX(S/T): 2
MGPSTPLLILFLLWSGPLQGQQHHLVEYMERRLAALEERLAQCQDQSSRHAELRDFKNKM
LPLLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKGKGR
RNEKYDMVTDCGYTISQVRSMKILKRGFPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPR
RDFTLAMAARKASRVRVFPWVGTGQLVYGGFLYFARRPPGRPGGGEMENTLQLIKFH
RTVVVDSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCLAKLDPQTLDTEQ
QWDTPCPRENAAAFVICGTLYVVVNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAH
ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEEV
```

**Important features:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 177-180, 248-251

## **FIGURE 91**

P  
E  
G  
I  
S  
E  
P  
D  
P  
A  
C  
O  
D

GACAGCTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTGCCCTCCGCTACGCAG  
 AGCCTCTCCGTGGCTCCGCACCTTGAGCATTAGGCCAGTTCCTCTCTCTAATCCAT  
 CCGTCACCTCTCCTGTCATCCGTTCCATGCCGTGAGGTCCATTACAGAACACATCCATGG  
 CTCTCATGCTCAGTTGGTCTGAGTCTCCTCAAGCTGGATCAGGGCAGTGGCAGGTGTT  
 GGGCCAGACAAGCCTGTCCAGGCCTGGTGGGGGAGGACGCAGCATTCTCCTGTTCTGTC  
 TCCTAAGACCAATGCAGAGGCCATGGAAGTGCAGGTTCTCAGGGCCAGTTCTAGCGTGG  
 TCCACCTCTACAGGGACGGGAAGGACCAGCCATTATGCAGATGCCACAGTATCAAGGCAGG  
 ACAAAACTGGTGAAGGATTCTATTGCGGAGGGCGCATCTCTGAGGCTGGAAAACATTAC  
 TGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTCCAGTCTACTACCAGAACAGGCCA  
 TCTGGGAGCTACAGGTGTCAGCACTGGCTCAGTCCCTCTCATTCCATCACGGGATATGTT  
 GATAGAGACATCCAGCTACTCTGTCAGTCCTCGGGCTGGTCCCCCGGCCACAGCGAAGTG  
 GAAAGGTCCACAAGGACAGGATTGTCCACAGACTCCAGGACAAACAGAGACATGCATGGC  
 TGTTGATGTGGAGATCTCTGACCGTCCAAGAGAACGCCGGAGCATACTGTTCCATG  
 CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACTTTTCA  
 GCCTATATCGTGGCACCTGGCTACCAAAGTACTGGAATACTCTGCTGTGGCCTATTTTG  
 GCATTGTTGGACTGAAGATTCTTCTCCAAATTCCAGTGGAAAATCCAGGCGGAACGGAC  
 TGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCGGAAACACGCAGTGGAGGTGAC  
 TCTGGATCCAGAGACGGCTACCCGAAGCTCTGCGTTCTGATCTGAAAATGTAACCCATA  
 GAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTACAAGGAAGAGTGTGGTGGCT  
 TCTCAGAGTTCCAAGCAGGAAACATTACTGGGAGGTGGACGGAGGACACAATAAGGTG  
 GCGCGTGGAGTGTGCCGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTGTCTCCG  
 ATCATGGGTACTGGTCCTCAGACTGAATGGAGAACATTGTATTCACATTAAATCCCGT  
 TTTATCAGCGTCTTCCCCAGGACCCCACCTACAAAAAATAGGGTCTCCTGGACTATGAGTG  
 TGGGACCATCTCCTTCTCAACATAATGACCAGTCCCTTATTACCCCTGACATGTCGGT  
 TTGAAGGCTATTGAGGCCCTACATTGAGTATCCGTCCTATAATGAGCAAAATGGAACCTCC  
 ATAGTCATCTGCCAGTCACCCAGGAATCAGAGAAAGAGGCCCTTGGCAAAGGGCTCTGC  
 AATCCCAGAGACAAGAACAGTGAGTCCTCCTCACAGGCAACCACGCCCTCCCCAGGG  
 GTGAAATGTAGGATGAATCACATCCCACATTCTTCTTAGGGATATTAGGTCTCTCTCCA  
 GATCCAAAGTCCCGCAGCAGCCGCCAAGGTGGCTCCAGATGAAGGGGACTGGCCTGTCC  
 ACATGGGAGTCAGGTGTCATGGCTGCCCTGAGCTGGGAGGGAAAGAAGGCTGACATTACATT  
 AGTTGCTCTCACTCCATCTGGCTAAGTGTATCTGAAATACCACCTCTCAGGTGAAGAACCG  
 TCAGGAATTCCCATCTCACAGGCTGTGGTAGATTAAGTAGACAAGGAATGTGAATAATGC  
 TTAGATCTTATTGATGACAGAGTGTATCCTAATGGTTGTTCATTATATTACACTTCAGTA  
 AAAAAA

## **FIGURE 92**

MALMLSLVLSLLKLGSQWQVFGPDKPVQALVGEDAASFCLSPKTNAEAMEVRFFRGQFSS  
VVHLYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISSQSYYQK  
AIWELQVSALGSVPPLISITGYVDRDIQLCQSSGWFPRPTAKWKGPQGQDLSTDRTNRDMH  
GLFDVEISLTQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF  
FGIVGLKIFFSKFQWKIQAEWDWRKHGQAEELRDARKHAVEVTLDPETAHPKLCVSDLKTVT  
HRKAPQEVPHSEKRFRKSVASQSFQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTL  
PDHGWWVRLNGEHLYFTLNPRFISVFPPTPPTKIGVFLDYECGTISFFNINDQSLIYTLTC  
RFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASAIPETSNSESSSQATTPFLP  
RGEM

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 239-255

## **FIGURE 93**

GCGATGGTGCGCCCGTGGCGGCGGTGCGGAGGCTTCCTGGTCGGATTGCA  
 ACGAGGAGAAGATGACTGACCAACCGACTGGCTGAATGAATGGCGGAGCCGAGCGC  
CATGAGGGAGCTGCCGAGCTGGCGGCCCTGCCCTGTTGTGCTGCCGCCGCCGCC  
 CGCTCGCCTCAGCCGCTCGGCCGGGAATGTCACCGTGGCGGCCGCCGCC  
 GACGCGTCGCCGGCCCCGGTTGCGGGGCGAGCCAGCCACCCCTTCCCTAGGGCGACGGC  
 TCCCACGGCCCAGGCCGGGAGGACCAGGGCCCCCGCGGCCACCGTCCACCGACCCCTGGCTG  
 CGACTTCTCCAGCCCAGTCCCCGGAGACCACCCCTTTGGCGACTGCTGGACCCCTTTCC  
 ACCACCTTCAGGCGCCGCTGCCGCCCTGCCGACCACCCCTCGGCCGGAAACGCACTTC  
 GACCACCTCTAGGCGCCGACCAAGACCCGCGGCCGACCAACCCCTTCGACGACCAACTGGCCGG  
 CGCCGACCAACCCCTGTAGCACCACCGTACCGGCCACGACTCCCCGGACCCGACCC  
 GATCTCCCAGCAGCACAGCAACAGCAGCGCTCTCCCCACCCACCTGCCACCGAGGGCCCC  
 TTCGCCTCCTCCAGAGTATGTACTGCTCTGTGGTGAAGCCTGAATGTGAATCGCT  
 GCAACCAGACCACAGGGCAGTGTGAGTGTGGCCAGGTTATCAGGGCTTCAGTGAAACC  
 TGCAAAGAGGGCTTTACCTAAATTACACTCTGGCTCTGTGAGCCATGTGACTGTAGTCC  
 ACATGGAGCTCTCAGCATAACCGTCAACAGGTAAGAACAGAGGGTGGAACTGAAGTTATT  
 TTATTTAGCAAGGGAAAAAAAAGGCTGCTACTCTCAAGGACCATACTGGTTAAACAAAG  
 GAGGATGAGGGTCATAGATTACAAAATTTTATATACTTTATTCTTACTTTATATGT  
 TATATTAAATGTCAGGATTAAAAACATCTAATTACTGATTAGTTCTCAAAAGCACTAG  
 AGTCGCAATTTCCTGGATAATTCTGTAAATTCTCATGGAAAAAAATTATTGAAGAAT  
 AAATCTGCTTCTGGAAGGGCTTCAGGCATGAAACCTGCTAGGAGGTTAGAAATGTTCTT  
 ATGTTATTAAATACCATGGAGTTGAGGAATTGTTGTTGGTTATTCTCTCTA  
 ATCAAAATTCTACATTGTTCTGGACATCTAAAGCTAACCTGGGGTACCTAATT  
 TTTAACTAGTGGTAAGTAGACTGGTTACTCTATTACAGTACATTGAGACCAAAAG  
 TAGATTAAGCAGGAATTATCTTAAACTATTATGTTATTGGAGGTAAATTAAATCTAGTGG  
 ATAATGTAAGTCTAAGCATTGCCTGTACTGCACTGAAAGTAATTATTCTTGACCT  
 TATGTGAGGCATTGGCTTTGTGGACCCCAAGTCAAAAAACTGAAGAGACAGTATTAAAT  
 AATGAAAAAAATAATGACAGGTTAACTCAGTGTAACTGGGTATAACCCAAGATCTGCTGC  
 CACTTACGAGCTGTGTTCTGGCAAGTAATTCTTCACTGAGCTGTTCTCTCAAG  
 GTTGTGAGGATTAATGAGTTGATATATAAAATGCCTAGCACATGTCACTCAATTAA  
 TTCTGGTTGTTAAATTCAAAGGAATTATGGACTGAAATGAGAGAACATGTTAAAGA  
 ACTTTAGCTCCTGACAAAGAAGTGTAACTTACTGACTAAATATTAAATGCTTT  
 TAAATGATATTATACTGTTATGGAATTGTTGATCATATTGTTGAGTTATTAAAAATGTAGAAG  
 AGGCTGGCGCGGTGGCTCACGCCGTAACTCTAGCAGCTGGGAGGCCAGGGCGGGTGGAT  
 CACTTGAGGCCAGGAGTTCTAGATGAGCCTGGCCAGCACAGTGAACACCCGTCTACTAAA  
 AATACAAACAAATTAGCTGGCGTGGTGGCACACACCTGTAGTCCCAGCTACTCGGGAGGCT  
 GAGGCAGGAGAATCGGTTGAACCCGGGAGGTGGAGGTTGCACTGAGCTGAGATCGGCCACT  
 GCACTCCAGCCTGGTGAGAGAGGGAGACTCTGTCTAAAAAAAAAAAAAA

**FIGURE 94**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRSLPSLGGIALLCCAAAAAAVASAASAGNVTGGGGAAGQVDASPGPGLRGEPSHPFPRATA
PTAQAPRTGPPRATVHRPLAATSPAQSPEPPPLWATAGPSSTTFQAPLGPSPTTPAERTS
TTSQAPTRPAPTLSTTGPAVTPVATTVPAPTPRTPTPDLPSSNSSVLPTPPATEAPS
SPPPEYVCNCNVGSINVNRCNQTTGQCECRPGYQGLHCETCKEGFYLNYSGLCQPCDCSP
HGALSIPCNR
```

**Important features of the protein:****Signal peptide:**

amino acids 1-25

**N-glycosylation sites.**

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

**EGF-like domain cysteine pattern signature.**

amino acids 214-226.

**FIGURE 95**

TGC GGCG CAGT GTAG ACCT GGGAGG **AT**GGGCGGC TGCT GCTGGCTGCTTTCTGGCTTG  
TCTCGGTGCCAGGGCCAGGCCGTGTGGTTGGGAAGACTGGACCTGAGCAGCTCTGG  
CCCTGGTACGTGCTTGCGGTGGCCTCCCAGGGAAAAGGGCTTGCCATGGAGAAGGACATGAA  
GAACGTCGTGGGGTGGTGGTACCCCTCACTCCAGAAAACAACCTGCGGACGCTGTCCTCTC  
AGCACGGGCTGGGAGGGTGTGACCAGAGTGTATGGACCTGATAAAGCGAAACTCCGGATGG  
GTGTTGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCACCAACTCAGAGA  
CTATGCCATCATCTCACTCAGCTGGAGTTGGGACGAGCCCTAACACACCGTGGAGCTGT  
ACAGTCTGACGGAGACAGCCAGCCAGGAGGCCATGGGCTCTCACCAAGTGGAGCAGGAGC  
CTGGGCTTCCTGTACAG**TAG**CAGGCCAGCTGCAGAAGGACCTCACCTGTGCTCACAAAGAT  
CCTTCTGTGAGTGCTGCGTCCCCAGTAGGGATGGCGCCACAGGGTCTGTGACCTCGGCCA  
GTGTCCACCCACCTCGCTCAGCGGCTCCGGGCCAGCACCAAGCTCAGAATAAAGCGATT  
CACAGCA

## **FIGURE 96**

MGGLLLAFLALVSPRAQAVWLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVT  
LTPENNLRTLSSQHGLGGCDQSVMMDLIKRNSGWVFENPSIGVLELWVLATNFRDYAIIFTQL  
EFGDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

**Signal peptide:**

amino acids 1-20

bio 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20

**FIGURE 97**

AACAGACGTTCCCTCGGGCCCTGGCACCTTAACCCCAGACATGCTGCTGCTGCTGCC  
 CCTGCTCTGGGGAGGGAGAGGGCGGAAGGCAGACAAGTAAACTGCTGACGATGCAGAGTT  
 CCGTGACGGTGCAGGAAGGCCTGTGTCCATGTGCCCTGCTCCTCCTACCCCTCGCAT  
 GGCTGGATTTACCCCTGGCCCAGTAGTTCATGGCTACTGGTCCGGGAAGGGCCAATACAGA  
 CCAGGATGCTCCAGTGGCCACAAACAACCCAGCTGGCAGTGTGGGAGGAGACTCGGGACC  
 GATTCCACCTCCTGGGGACCCACATACCAAGAATTGCACCCGTAGCAGAGATGCCAGA  
 AGAAGTGATGCGGGAGATACTTCTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAA  
 ACATCACCGGCTCTGTGAATGTGACAGCCTGACCCACAGGCCAACATCCTCATCCCAG  
 GCACCCCTGGAGTCCGGCTGCCCTCAGAACATCTGACCTGCTCTGTGCCCTGGCCTGTGAGCAG  
 GGGACACCCCCATGATCTCCTGGATAGGGACCTCCGTGTCCCCCTGGACCCCTCCACCAC  
 CCGCTCCTCGGTGTCACCCATCCCACAGCCCCAGGACCATGGCACCCAGCCTCACCTGTC  
 AGGTGACCTTCCCTGGGCCAGCGTGACCACGAACAAGACCGTCCATCTAACGTGTCC  
 CCGCCTCAGAACTTGACCATGACTGTCTCCAAGGAGACGGCACAGTATCCACAGTCTGGG  
 AAATGGCTCATCTGTCACTCCCAGAGGCCAGTCTCTGCGCCTGGTCTGTGCAGTTGATG  
 CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCCTGACCCCTGTCCCC  
 TCACAGCCCTCAAACCCGGGGTGCTGGAGCTGCCCTGGTGCACCTGAGGGATGCAGCTGA  
 ATTACACCTGCAGAGCTCAGAACCCCTCTGGCTCTCAGCAGGTCTACCTGAACGTCTCC  
 AGAGCAAAGCCACATCAGGAGTGACTCAGGGGTGGTCGGGGAGCTGGAGGCCACAGCC  
 GTCTTCCCTGCCTCTGCGTCATCTCGTTGAGGTCTGCAGGAAGAAATCGGCAAG  
 GCCAGCAGCGGGCGTGGAGATAAGGGCATAGAGGATGCAAACGCTGTCAGGGGTTCA  
 CTCAGGGGCCCTGACTGAACCTGGCAGAACAGACTCCCCAGACCGCCTCCCCAGCT  
 TCTGCCGCTCCTCAGTGGGGAGGAGAGCTCCAGTATGCATCCCTCAGCTCCAGATGGT  
 GAAGCCTGGGACTCGGGGACAGGAGGCCACTGACACCCGAGTACTCGGAGATCAAGATCC  
 ACAGATGAGAAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCTCCAGGCAAGGG  
 GAAGTCAGAGGCTGATTCTGTAGAATTAAACAGCCCTAACGTGATGAGCTATGATAAC  
 ATGAATTATGTGCAGAGTGAAAAGCACACAGGCTTAGAGTCAAAGTATCTAAAC  
 CCACACTGTGCCCTCCCTTTATTTTTAACTAAAAGACAGACAAATTCTA

## **FIGURE 98**

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPSCFSYPSHGWIYPGPVVHGYWF  
REGANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLISRARRSDAGRYFFRMEKG  
SIKWNYKHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCSPWACEQGTPPMISWIGTSVS  
PLDPSTTRSSVLTLPQPQDHGTSLTCQVTFPGASVTTNKTVHLNVSYPPQNLTMVFQGDG  
TVSTVLGNSSSLPEGQSLRLVCAVDADSNPPARLSLSWRGLTLCPSQPSNPGVLELPWV  
HLRDAAEFTCRAQNPLGSQQVYLNVSLQSKATSGVTQGVVGGAGATALVFLSFCVIFVVVR  
CRKKSARPAAGVGDTGIEDANAVRGSAASQGPLTEPWAEDSPPDQPPPASARSSVGEGELOQYA  
SLSFQMVKPWDSRGQEATDTEYSEIKIHR

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 351-370

**FIGURE 99**

GACGCCAGTGACCTGCCGAGGTGGCAGCACAGAGCTCTGGAGATGAAAGACCCTGTTCTG  
GGTGTACGCTCGGCCTGGCCGCTGCCCTGTCCTCACCCCTGGAGGAGGAGGATATCACAGG  
GACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTCCGGAGGACAGGAGGCCAGGA  
AGGTGTCCCCAGTGAAGGTGACAGCCCTGGCGGTGGAAAGTTGGAAGGCCACGTTCACCTTC  
ATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAGCCTGGCAA  
ATACAGCGCCTATGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCAGGAGGGACCACT  
ACATCTTTACTGCAAAGACCAGCACCATGGGGCCTGCTCCACATGGAAAGCTTGTGGGT  
AGGAATTCTGATACCAACCAGGGAGGCCCTGGAAGAATTAAAGAAATTGGTGCAGCGCAAGGG  
ACTCTCGGAGGAGGACATTTCACGCCCTGCAGACGGGAAGCTGCCTTCCCACACTAGG  
CAGCCCCGGGTCTGCACCTCCAGAGCCCACCCCTACCACCAAGACACAGGCCGGACCACT  
GGACCTACCCCTCCAGCCATGACCCCTCCCTGCTCCCACCCACCTGACTCCAAATAAGTCCT  
TTTCCCCAA

## **FIGURE 100**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65404
<subunit 1 of 1, 170 aa, 1 stop
<MW: 19457, pI: 9.10, NX(S/T): 0
MKTLFGLGVTLGLAAALSFTLEEEEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGGKL
EATFTFMREDRCIQKKILMRKTEEPGKYSAYGGRKLMYLQELPRRDHYIFYCKDQHHGGLLH
MGKLVGRNSDTNREALEEFKKLVQRKGLSEEDIFTPLQTGSCVPEH
```

**Important features:**

**Signal peptide:**

amino acids 1-17

**FIGURE 101**

GTTCCGCAGATGCAGAGGTTGAGGTGGCTCGGGACTGGAAGTCATCGGCAGAGGTCTCAC  
AGCAGCCAAGAACCTGGGCCCGCTCCTCCCCCTCCAGGCCATGAGGATTCTGCAGTTAA  
TCCTGCTTGCTCTGGCAACAGGGCTTGTAGGGGGAGAGACCAGGATCATCAAGGGGTCGAG  
TGCAAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTCGAGAAGACGCGGCTACTCTGTGG  
GGCGACGCTCATGCCCAAGATGGCTCCTGACAGCAGCCACTGCCTCAAGCCCCGCTACA  
TAGTTCACCTGGGCAGCACAACCTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAGCC  
ACTGAGTCCTCCCCCACCCGGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGA  
CATCATGCTGGTGAAGATGGCATGCCAGTCTCCATCACCTGGCTGTGCGACCCCTCACCC  
TCTCCTCACGCTGTGTCAGTGGCACCAGCTGCCCTATTCCGGCTGGGCAGCACGTCC  
AGCCCCCAGTTACGCCCTGCCTCACACCTTGCATGCGCAACATCACCATCATTGAGCACCA  
GAAGTGTGAGAACGCCTACCCGGCAACATCACAGACACCATGGTGTGCCCCAGCGTGCAGG  
AAGGGGGCAAGGACTCCTGCCAGGGTGAUTCCGGGGCCCTCTGGTCTGTAACCAGTCTTT  
CAAGGCATTATCTCCTGGGCCAGGATCCGTGTGCGATCACCGAAAGCCTGGTGTACAC  
GAAAGTCTGCAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAATAGACTGGACCCA  
CCCACACCAGCCATCACCCCTCATTCCACTTGGTGTGTTGGTCTGTTCACTCTGTTAAT  
AAGAAACCTAAGCCAAGACCCCTACGAACATTCTTGGCCTCTGGACTACAGGAGATG  
CTGTCACTTAATAATCAACCTGGGTTGAAATCAGTGAGACCTGGATTCAAATTCTGCCCT  
GAAATATTGTGACTCTGGGAATGACAACACCTGGTTGTTCTGTGTATCCCCAGCCCCA  
AAGACAGCTCCTGGCCATATCAAGGTTCAATAAATATTGCTAAATGAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 102**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405
<subunit 1 of 1, 250 aa, 1 stop
<MW: 27466, pI: 8.87, NX(S/T): 4
MRILQLILLALATGLVGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLAAH
CLKPRYIVHLGQHNLQKEEGCEQRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSITW
AVRPLTLSSRCVTAGTSCLISGWGSTSSPQLRLPHTLRCANITIEHQKCENAPGNITDTM
VCASVQEGGKDSCQGDGGPLVCNQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKNN
```

**Important features:**

**Signal peptide:**

amino acids 1-18

**Serine proteases, trypsin family, histidine active site.**

amino acids 58-63

**N-glycosylation sites.**

amino acids 99-102, 165-168, 181-184, 210-213

**Glycosaminoglycan attachment site.**

amino acids 145-148

**Kringle domain proteins.**

amino acids 197-209, 47-64

**Serine proteases, trypsin family, histidine protein**

amino acids 199-209, 47-63, 220-243

**Apple domain proteins**

amino acids 222-249, 189-222

**FIGURE 103**

GAGCAGTGTCTGCTGGAGCCG**ATG**CCAAAACCATGCATTCTTATTCA  
GAGATTCATTGTTTCTTTATCTGTGGGCCTTTACTGCTCAGAGACAAAGAAAGAGGAGAGC  
ACCGAAGAAAGTAAAGAGCTCATCGTCCAGAAAAGTCTAAGACAAGCAAGAAGGGAGAC  
ACTAAATGCCATTATGACGGCTACCTGGCTAAAGACGGCTCGAAATTCTACTGCAGCC  
CACAAAATGAAGGCCACCCAAATGGTTGTTCTGGTGGCAAGTCATAAAAGGC  
GACATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGTAGTTAC  
TACCCCCTTCATTGCTACGGAAAGGAAGGCTATGCAGAAGGCAAGATTCCAC  
CGGATGCTACATTGATTGATTTTGAGATTGAACTTTATGCTGTGAC  
CAAAGGACCACGGAGCATTGAGACATTAAACAAATAGAC  
ATGGACAATGACAGGCAGCTCTCTAAAGCCGAGATAAACCTCTACTTG  
CAAAGGGATTGAAAGATGAGAACGACGTGACAAGTCATATCAG  
GATGCAGTTAGAAGATATTTTAAGAAGAATGACCATGATGGT  
GATGGCTTCATTCTCCAAGGAATACAATGTATACCAACACGAT  
GAACTA**TAG**CATATTTGTATTTCTACTTTTTTTAGCTATT  
ACTGTACTTTATGTATAAACAAAGTCAC  
TTTCTCCAAGTTGCTATTGCTATT  
TTCCCCTATGAGAAGATATTTGA  
TCTCCCCAATACATTGATTTGGTATAATAAATGTGAGGCT  
GTTTGCAAACTTAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 104**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406
<subunit 1 of 1, 222 aa, 1 stop
<MW: 25794, pI: 6.24, NX(S/T): 1
MPKTMHFLFRFIVFFYLWGLFTAQRQKKEESTEEVKIEVLHRPENCSKTSKKGDLLNAHYDG
YLAKDGSKFYCSRTQNEGHPKWVLGVGQVIKGLDIAMTDMCPGEKRKVVIPPSFAYGKEGY
AEGKIPPDATLIFEIELYAVTKGPRSIETFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD
KSYQDAVLEDIFKKNDHDGDFISPKEYNVYQHDEL
```

**Important features:**

**Endoplasmic reticulum targeting sequence.**

amino acids 219-222

**N-glycosylation site.**

amino acids 45-48

**FKBP-type peptidyl-prolyl cis-trans isomerase**

amino acids 87-223, 129-142

**EF-hand calcium-binding domain proteins**

amino acids 202-214, 195-214

**FIGURE 105**

CAGAA**ATG**CAGGGACCATTGCTTCTTCCAGGCCTCTGCTTCTGCTGAGCCTCTTGGAGCT  
GTGACTCAGAAAACCAAAACTCCTGTGCTAAGTGCCCCCAAATGCTTCTGTGTCAATAA  
CACTCACTGCACCTGCAACCATGGATATACTTCTGGATCTGGCAGAAACTATTCACATTCC  
CCTTGGAGACATGTAACGCCAGGCATGGTGGCTCGCGCTG**TAA**TCCAGTTCTTGGGAAG  
CCAAGGCAGGTGGATCACCTGAGGTCAAGGAGTTGAGACCAGCCTGGCCAACATAGTGAAAC  
CCC GTGTCTACTAAAAATACAAAAATCAGCCGGCGTGGTGGTGCATGCCTGCAATCCCAGT  
TACTCGGGAGGCTGAGGCAGGAGAATCGCTGAACTCAGGAGGCAGAAGTTGCAGTGAACCC  
AGATCCTGCCATTGCACTCCAGCATGGATGACAGAGCAAGACTCCGTCTCAAAAAGAAAAGA  
TAGTTCTTGTTCATT CGCGACTGCCCTCTCAGTGTTCCTGGATCCCCTCCAAATAA  
AGTACTTATATTCTC

## **FIGURE 106**

MQGPILLPGLCFLLSLFGAVTQKTKTSCAKCPPNASCVNNTHCTCNHGYTSGSGQKLFTFPL  
ETCNARHGGSR

**Signal peptide:**

amino acids 1-18

**FIGURE 107**

CAAGCAGGT CATCCCCTGGTGACCTCAAAGAGAAGCAGAGAGGGCAGAGGTGGGGGCAC  
AGGGAAAGGGT GACCTCTGAGATTCCCCTTCCCCAGACTTGGAAAGT GACCCACC**ATGG**  
GGCTCAGCATTTTGCTCCTGTGTGTTGGGCTCAGCCAGGCAGCCACACCGAAGATT  
TTCAATGGCACTGAGTGTGGCGTA ACTCACAGCCGTGGCAGGTGGGCTGTTGAGGCAC  
CAGCCTGCCTGC GGGGGTGTCCTATTGACCACAGGTGGGCTC ACAGCGGCTCACTGCA  
GCGGCAGCAGGTACTGGGTGCGCCTGGGGAACACAGCCTCAGCCAGCTGACTGGACCGAG  
CAGATCCGGCACAGCGGCTCTGTGACCCATCCGGTACCTGGGAGCCTCGACGAGCCA  
CGAGCACGACCTCCGGCTGCTGCCCTGCCCTGCCGTCCCGTAACCAGCAGCGTTCAAC  
CCCTGCCCTGCCCAATGACTGTGCAACCCTGGCACCGAGTGCCACGTCTCAGGCTGGGC  
ATCACCAACCACCCACGGAACCCATTCCGGATCTGCTCCAGTGCCTCAACCTCTCCATCGT  
CTCCCATGCCACCTGCCATGGTGTATCCCGGGAGAACATCAGGAGAACATGGTGTGAG  
GCGCGTCCGGGCAGGATGCCCTGCCAGGGTGATTCTGGGGCCCTGGTGTGAG  
GTCCTCAAGGTCTGGTGCCTGGGGTCTGTGGGCCCTGTGGACAAGATGGCATCCCTGG  
AGTCTACACCTATATTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACAA**TGAC**  
CTGTTCCCTCCACCTCCACCCCCACCCCTTAACCTGGGTACCCCTGGCCCTCAGAGCACC  
AATATCTCCTCCATCACTCCCTAGCTCCACTCTGTTGCCCTGGAACTTCTTGGAACTT  
TAACTCCTGCCAGCCCTCTAAGACCCACGAGCAGGGTGAGAGAAGTGTGCAATAGTCTGGA  
ATAAAATATAAATGAAGGGAGGGGCAAAAAAAAAAAAAAAA

## **FIGURE 108**

MGLSIFLLLCLVGLSQATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAH  
CSGSRYWVRLGEHSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLRLPVRVTSSV  
QPLPLPNDCATAGTECHVSGWGITHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVC  
AGGVPGQDACQGDGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWIRMIMRNN

**Signal peptide:**

amino acids 1-17

bio 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249

**FIGURE 109**

GC GGCCACACG CAGCTAGCCGGAGCCC GACCAGGC GCGCTGTGCCTCCTCGTCCCTCGC  
 CGCGTCCCGAAGCCTGGAGCCGGCGGGAGCCCCCGCGCTGCC **ATGT** CGGGCGAGCTCAGCA  
 ACAGGTTCCAAGGAGGGAAAGGCGTTGGCTTGCTCAAAGCCGGCAGGAGAGGAGGCTGGCC  
 GAGATCAACCGGGAGTTCTGTGACCAAGAAGTACAGTGATGAAGAGAACCTCCAGAAAA  
 GCTCACAGCCTCAAAGAGAAGTACATGGAGTTGACCTGAACAATGAAGGCGAGATTGACC  
 TGATGTCTTAAAGAGGATGATGGAGAAGCTGGTGTCCCCAAGACCCACCTGGAGATGAAG  
 AAGATGATCTCAGAGGTGACAGGAGGGTCAGTGACACTATATCCTACCGAGACTTGTGAA  
 CATGATGCTGGGAAACGGTCGGCTGCC CAAGTTAGTCATGATGTTGAAGGAAAAGCCA  
 ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCTCCAGAGAGACATTGCTAGCCTGCC **TGA**  
 GGACCCCGCCTGGACTCCCCAGCCTCCCACCCATA CCTCCCTCCGATCTGCTGCCCTT  
 CTTGACACACTGTGATCTCTCTCTCATTTGTTGGTATTGAGGGTTTGTGTT  
 TCATCAATGTCTTGTAAAGCACAAATTATCTGCCTTAAAGGGCTCTGGTCGGGAATCC  
 TGAGCCTTGGTCCCCTCCCTCTCTTCTCCCTCCCCGCTCCGTGCAGAAGGGCTG  
 ATATCAAACCAAAACTAGAGGGGGCAGGGCCAGGGCAGGGAGGCTTCCAGCCTGTGTTCCC  
 CTCACTTGGAGGAACCAGCACTCTCCATCCTTCAGAAAGTCTCCAAGCCAAGTTCAGGCTC  
 ACTGACCTGGCTCTGACGAGGACCCCAGGCCACTCTGAGAAGACCTGGAGTAGGGACAAGG  
 CTGCAGGGCCTTTGGGTTCTGGACAGTGCATGGTCCAGTGCTCTGGTGTACCC  
 AGGACACAGCCACTCGGGGCCCGCTGCCAGCTGATCCCCACTCATTCCACACCTCTTCT  
 CATCCTCAGTGATGTGAAGGTGGAAAGGAAAGGAGCTGGCATTGGAGGCCCTCAAGAAGG  
 TACCAAGGAACCCCTCCAGTCCTGCTCTGCCACACCTGTGCAGGCAGCTGAGAGGCAG  
 CGTGCAGCCCTACTGTCCCTACTGGGGCAGCAGAGGGCTCGGAGGCAGAAGTGAGGCC  
 GGGTTGGGGAAAGGTCAAGTCAGTGCTGTTCCACCTTGTAGGGAGGACTGAGGGAC  
 CAGGATGGGAGAATGAGGAGTAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA  
 CTGAGAAATACAAGGTTGCTGTGACCCCAATCTGCTGAAAAA

4 3 2 6 5 4 0 \* 1 2 1 2 0 1

## **FIGURE 110**

MSGELSNRFQGGKAFGLLKARQERRLAEINREFLCDQKYSDEENLPEKLTAKEKYMEFDLN  
NEGEIDLMSLKRMMEKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMMLGKRSAVLKLVM  
MFEGKANESSPKPVGPPPERDIASLP

## **FIGURE 111A**

CGCGCTCCCCGCGCCTCCTCGGGCTCCACCGTCTTGCCTCGAGAGGCAGGCCCTCCA  
 GGAGCGGGGCCCTGCACACC**ATG**GCCCCCGGGTGGCAGGGTGGCGCCGTGCGGCC  
 CGCCTGGCGCTGGCCTGGCGCTGGCGAGCGTCTGAGTGGCCTCCAGCCGTGCGCTGCC  
 CACCAAGTGTACCTGCTCCGCTGCCAGCGTGGACTGCCACGGCTGGCCTCCGCGCGGTT  
 CTCGGGGCATCCCCGCAACGCTGAGCGCCTTGACCTGGACAGAAATAATATCACCAAGGATC  
 ACCAAGATGGACTTCGCTGGCTCAAGAACCTCCGAGTCTGCATCTGAAGAACAAACCAGGT  
 CAGCGTCATCGAGAGAGGGCGCTTCCAGGACCTGAAGCAGCTAGAGCGACTGCGCCTGAACA  
 AGAATAAGCTGCAAGTCTTCCAGAATTGCTTTCCAGAGCACGCCAAGCTCACCAAGACTA  
 GATTGAGTAAAACCAGATCCAGGGATCCCAGGAAGGCGTCCCGGGCATACCGATGT  
 GAAGAACCTGCAACTGGACAACAACCACATCAGCTGCATTGAAGATGGAGCCTTCCGAGCGC  
 TGCGCGATTGGAGATCCTTACCCCTAACAAACAACATCAGTCGATCCTGGTCACCAGC  
 TTCAACCACATGCCGAAGATCCGAACCTGCGCCTCCACTCCAACCACCTACTGCGACTG  
 CCACCTGGCCTGGCTCTGGATTGGCTGGACAGGGACAGTTGGCCAGTTCACACTCT  
 GCATGGCTCCTGTGCATTGAGGGCTTCAACGTGGCGGATGTGCAGAAGAAGGAGTACGTG  
 TGCCCAGCCCCCCTCGGAGCCCCATCCTGCAATGCCAACTCCATCTCCTGCCCTCGCC  
 CTGCACGTGCAGCAATAACATCGTGGACTGTCGAGGAAGGGCTTGATGGAGATTCTGCCA  
 ACTTGGCGGAGGGCATCGTCAAACAGCCTAGAACAGAACTCCATCAAAGCCATCCCTGCA  
 GGAGCCTTCACCCAGTACAAGAAACTGAAGCGAATAGACATCAGCAAGAATCAGATATCGGA  
 TATTGCTCCAGATGCCTCCAGGGCTGAATCACTCACATCGTGGCTGTATGGGAACA  
 AGATCACCGAGATTGCCAAGGGACTGTTGATGGCTGGTGTCCCTACAGCTGCTCCTCCTC  
 AATGCCAACAAAGATCAACTGCCTGCGGGTGAACACGTTTCAAGGACCTGCAGAACCTCAACTT  
 GCTCTCCCTGTATGACAACAAGCTGCAGACCATCAGCAAGGGCTTCTCGCCCTCTGCACT  
 CCATCCAGACACTCCACTTAGCCAAAACCCATTGTGTGCAGTGCCTTAAGTGGCTG  
 GCCGACTACCTCCAGGACAACCCATCGAGACAAGCGGGGCCGCTGCAGCAGCCGCC  
 ACTCGCCAACAAGCGCATGCCAGATCAAGAGCAAGAAGTTCCGCTGCTCAGGCTCCGAGG  
 ATTACCGCAGCAGGTTCAGCAGCGAGTGCTCATGGACCTCGTGTGCCCTGAGAAGTGTG  
 TGTGAGGGCAGATTGGACTGCTCCAACCAGAACGCTGGTCCGATCCCAAGGCCACCTCCC  
 TGAATATGTCACCGACCTGCACTGAATGACAATGAGGTATCTGTTCTGGAGGCCACTGGCA  
 TCTTCAAGAAGTTGCCAACCTGCGGAAAATAATCTGAGTAACAATAAGATCAAGGAGGTG  
 CGAGAGGGAGTTCGATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGACAGGGAACCAGCT  
 GGAGACCGTGACGGCGCTGTTCCGTGGCCTCAGTGGCCTAAAACCTTGATGCTGAGGA  
 GTAACCTGATCAGCTGTTGAGTAATGACACCTTGCCGGCTGAGTTGGTGGAGACTGCTG  
 TCCCTCTATGACAATCGGATCACCACCATCACCCTGGGGCCTTCACCACGCTTGTCTCCCT  
 GTCCACCATAAACCTCGTCCAACCCCTCAACTGCAACTGCCACCTGGCCTGGCTCGGCA  
 AGTGGTTGAGGAAGAGGGGGATCGTCAGTGGAACCCCTAGGTGCCAGAACCCATTTCCTC  
 AAGGAGATTCCCATCCAGGATGTGGCCATCCAGGACTTCACCTGTGATGGCAACGAGGAGAG  
 TAGCTGCCAGCTGAGCCCGCTGCCGGAGCAGTGCACCTGTATGGAGACAGTGGTGCAG  
 GCAGCAACAAGGGGCTCCCGCCCTCCCCAGAGGCATGCCCAAGGGATGTGACCGAGCTGTAC  
 CTGGAGGAAACCACCTAACAGCGTGCAGAGAGCTGTCGCCCTCCGACACCTGACGCT  
 TATTGACCTGAGCAACAACAGCATCAGCATGCTGCCAATTACACCTTCAGTAACATGTCTC  
 ACCTCTCCACTCTGATCTGAGCTACAACCGGCTGAGGTGCATCCCCGTCCACGCCCTCAAC  
 GGGCTGCGGTCCCTGCGAGTGCTAACCCCTCATGGCAATGACATTCCAGCGTCTGAAGG  
 CTCCCTCAACGACCTCACATCTTCCCATCTGGCGTGGGAACCAACCCACTCCACTGTG  
 ACTGCAGTCTCGGTGGCTGCGAGTGGTGAAGGCAGGGTACAAGGAGCCTGGCATCGCC  
 CGCTGCAGTAGCCCTGAGGCCATGGCTGACAGGCTCTGCTACCACCCAAACCCACCGCTT  
 CCAGTGCAAAGGGCCAGTGGACATCAACATTGTGGCCAAATGCAATGCCCTGCCTCCAGCC  
 CGTGCAAGAATAACGGGACATGCACCCAGGACCCTGTGGAGCTGTACCGCTGTGCCCTGCC

## **FIGURE 111B**

TACAGCTACAAGGGCAAGGACTGCACTGTGCCATCAACACCTGCATCCAGAACCCCTGTCA  
 GCATGGAGGCACCTGCCACCTGAGTGACAGCCACAAGGATGGGTTAGCTGCTCCTGCCCTC  
 TGGGCTTGAGGGGCAGCGGTGTGAGATCAACCCAGATGACTGTGAGGAACAGACTGCGAA  
 AACAAATGCCACCTGCGTGGACGGATCAACAACATACGTGTATCTGTCCGCCACTACAC  
 AGGTGAGCTATGCGACGGAGGTGATTGACCACTGTGTGCTGAGCTGAACCTCTGTCAGCATG  
 AGGCCAAGTGCATCCCCCTGGACAAAGGATTCAAGCTGCGAGTGTGTCCTGGCTACAGCGGG  
 AAGCTCTGTGAGACAGACAATGATGACTGTGCCCCACAAGTGCCGCCACGGGGCCAGTG  
 CGTGGACACAATCAATGGCTACACATGCACCTGCCCAAGGGCTTCAGTGGACCCTTGTG  
 AACACCCCCCACCCATGGCCTACTGCAGACCAGCCATGCGACCAGTACGAGTGCCAGAAC  
 GGGGCCAGTGCATCGGGTGCAGCAGGAGCCCACCTGCCGCTGCCACCAGGCTTCGCCGG  
 CCCCAGATGCGAGAAGCTCATCACTGTCAAACCTCGTGGGCAAAGACTCCTACGTGGAACGTGG  
 CCTCCGCCAAGGTCCGACCCCAAGGCCAACATCTCCCTGCAGGTGGCCACTGACAAGGACAAC  
 GGCATCCTCTCTACAAAGGAGACAATGACCCCCCTGGCACTGGAGCTGTACCGAGGCAACGT  
 GCGGCTGGTCTATGACAGCCTGAGTTCCCTCAACCACAGTGTACAGTGTGGAGACAGTGA  
 ATGATGGGCAGTTCACAGTGTGGAGCTGGTACGCTAAACCAGACCCCTGAACCTAGTAGTG  
 GACAAAGGAACCTCAAAGAGCCTGGGAAGCTCCAGAAGCAGCCAGCAGTGGCATCAACAG  
 CCCCCTCTACCTTGGAGGCATCCCCACCTCCACGGGCTCTCCGCCCTGCGCCAGGGCACGG  
 ACCGGCCTCTAGGCCTCCACGGATGCATCCATGAGGTGCGCATCAACAAACGAGCTGCG  
 GACTTCAAGGCCCTCCACACAGTCCCTGGGGTGTACCCAGGCTGCAAGTCCGTGACCGT  
 GTGCAAGCAGGCCCTGTGCCGCTCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGCCGCCAG  
 GCTGGACCAGGCCACTCTGCAGACCAGGAGGCCGGACCCCTGCCTCGGCCACAGATGCCAC  
 CATGGAAAATGTGTGGCAACTGGACCTCATACTGTGCAAGTGTGCCGAGGGCTATGGAGG  
 GGACTTGTGTGACAACAAGAATGACTCTGCCAATGCCCTGCTCAGCCTCAAGTGTGACCATG  
 GGCAGTGCCACATCTCAGACCAAGGGAGCCCTACTGCCGTGCCAGCCGGCTTAGCGGC  
 GAGCACTGCCAACAAAGAGAACCGTGCCTGGGACAAGTAGTCCGAGAGGTGATCCGCC  
 GAAAGGTTATGCATCATGTGCCACAGCCTCCAAGGTGCCCATCATGGAATGTCGTGGGGCT  
 GTGGGCCCTGGCTGCTGCCAGGCCACCCGCAGCAAGCGCGGAAATACGTCTCCAGTGCACG  
 GACGGCTCCTCGTTGAGAAGAGGTGGAGAGACACTTAGAGTGCCTGCCGTGCGTGTTC  
 CTAAGGCCCTGCCGCCCTGCCACCTCTCGACTCCAGCTTGATGGAGTTGGACAGCC  
 ATGTGGACCCCTGGTGATTGACATGAAGGAAATGAAGGCTGGAGAGGAAGGTAAAGAAGA  
 AGAGAATATTAAGTATTTGTAACAAAAAATAGAACTTAAAAAAAAAAAAAAA  
 AAAAAA

## **FIGURE 112**

MAPGWAGVGA AVRARLALALASVL SGPPAVACPTKCTCSAASVDCHGLGLRAVPRGIPRN  
 AERLDLDRNNITRITKMDFAGLK NL RVLHLEDNQSVIERGAFQDLKQLERLRLNKNKLQVL  
 PELLFQSTPKLTRL DLS ENQI QGIPRKAFRGITDVKNLQLDNHHIS CIEDGAFRALRDLEIL  
 TLNNNNISRI LVT SFNHMPKIRTLRLHSNHL YCDCHLAWLSDWLRQRRTVGQFTLCMAPVHL  
 RGFNVADVQKKEYVC PAP HSEPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPEGIV  
 EIRLEQNSIKAI PAGAFTQYKKLKRIDISK NQISDIAPDAFQGLKS LTSLVLYGNKITEIAK  
 GLFDGLVSLQ LLLNANKINCLRVNTFQDLQNLNLLS LYDNKLQTISKGLFAPLQSIQTLHL  
 AQNP FVCDCHLKWLADYLQDNPIETSGARCSSPRRLANKRISQIKSKKFRCSGSEDYRSRFS  
 SEC FM DLVCPEKCRCEGTIVDCSNQKLVRIPSHLPEYVTDLRLNDNEVS VLEATGIFKKLPN  
 LRKINLSNNKI KEVREGA FDGA ASVQELMLTGNQLET VHGRVFRGLS GLKTLM RSNL I SCV  
 SNDT FAGLSSVRLLS LYDNRITTITPGAF TTLVSLSTINLLS NPFCNCNCHLAWLGKWL RKR  
 IVSGNPRCQKPF FLKEI PIQDVAI QDFTCDGNEESSCQLSPRCPEQCTCMETVVRC SNKGLR  
 ALPRGMPKDVT ELYLEG NHTAVPRELSALRHLTLIDLSNNS ISMLTN YTFSNM SHLSTL  
 SYNRLRCIPVHAFNGLRS LRVL TLHGNDI SSVPEGSFNDLTSLSHIALGTNPLHCDCSR WL  
 SEWVKAGYKEPGI ARCSSPEPMADRL LTTPTHRFQCKGPVDINIVAKCNACLSSPCKNN GT  
 CTQDPVELYRCACPYSYKGKDCTVPINTCIQNPCQHGGTCHLSDSHKDGFSCSCPLGEGQR  
 CEINPDDCEDND CENNATCVDGINNYVCICPPNYTGELCDEVIDHC VP ELNLCQHEAKC I PL  
 DKGF SCECVPGYSGKLCETDNDDCVAHKCRHGAQCVD TINGYTCTCPQGFSGPFCEHPPP MV  
 LLQTSPCDQYECQNGAQ CIVVQQEPTCRCP PGFAGPRCEK LITVNFGKDSYVELASAKVR P  
 QANISLQVATDKDNGILLYKGNDPLA LE LYQGHVRLVYDSLSSP TT VY SVETVNDQF HS  
 VELVTLNQTLNLVVDKGTPKSLGKLQPAVGINSPLY LGGIPTSTGLS ALRQGTDRPLGG F  
 HGCIHEVRINN ELQDFKALPPQSLGVSPGCKSCTVCKHGLCRSVEKDSV VCECRPGWTGPLC  
 DQEARDPCIGHRCHHGKVATGT SYMCKCAEGYGGDLC DNKN DSANACSAFKCHHGQCHI SD  
 QGEPYCLCQPGFSGEHCQQENPCLGQVVREVIRRQKG YASCATASKV PIMECRGGCGPQCC Q  
 PTRSKRRKYVFQCTDGSSFVEVERHLECGCLACS

**Signal peptide:**

amino acids 1-27

**FIGURE 113**

GGATGCAGGACGCTCCCTGAGCTGCCTGTCAACGACTAGGTGGAGCAGTGTTCCTCCGCA  
GACTCAACTGAGAAGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTCAGTTCTGTCT  
CCGGCAGGCTTGAGG**ATG**AAGGCTGCAGGCATTCTGACCCCTCATGGCTGCCGGTACAG  
GCGCCGAGTCCAAAATCTACACTCGTTGCAAACGGCAAAATATTCTCGAGGGCTGGCCTG  
GACAATTACTGGGCTTCAGCCTGGAAACTGGATCTGCATGGCATATTATGAGAGCGGCTA  
CAACACCACAGCCCCGACGGCCTGGATGACGGCAGCATCGACTATGGCATCTCCAGATCA  
ACAGCTTCGCGTGGTGCAGACCGGAAAGCTGAAGGAGAACAAACCACTGCCATGTCGCCTGC  
TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAATTGTTAAAGA  
GACACAAGGAATGAACATTGGCAAGGCTGGAAGAACATTGTGAGGGCAGAGACCTGTCCG  
AGTGGAAAAAAGGCTGTGAGGTTCC**TAA**ACTGGAACGGACCCAGGATGCTTGCAGAAC  
GCCCTAGGATTGCAGTGAATGTCAAATGCCTGTGTACCTGTCCCCTTCCCTCCAAATA  
TTCCTTCTCAAACGGAGAGGGAAAATTAGCTATACTTTAAGAAAATAATTTCCAT  
TTAAATGTC

## **FIGURE 114**

MKAAGILTLLIGCLVTGAESKIIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAP  
TVLDDGSIDYGIFQINSFAWCRRGKLKENNHCCHVACSLITDDLTDATTCARKIVKETQGMN  
YWQGWKKHCEGRDLSEWKKGCEVS

**Signal peptide:**

amino acids 1-19

## **FIGURE 115**

CAGGCCATTCGATCCACTGTCCTTGTGGAGCCAGGCCACACCGTCCTCAGCAGTGT  
 CATGTGTTAAAACGCCAAGCTGAATATATC**ATG**CCCCTATTAAACTTGTACATGGCTCCC  
 CATTGGTTTGAGAAAAGTCAAGCTTTACCTGGTCTGCCTGTATCCCAGTGTTC  
 AGGCTGGCTAGACGGCGGAAGAAGATCCTATTTACTGTCACCTCCAGATCTGCTTCAC  
 CAAGAGAGATTCTTCTAAACGACTATAACAGGGCCCCAATTGACTGGATAGAGGAATACA  
 CCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTCACAGCTGCTGTTTAAGGAA  
 ACATTCAAGTCCCTGTCACATAGACCTGATGTCCTCTATCCATCTCAAATGTCACCAG  
 CTTGACTCAGTTGTCCTGAAAAGCTGGATGACCTAGTCCCAAGGGAAAAATTCCCTGC  
 TGCTCTCCATCAACAGATAAGGAAAGAAAAATCTGACTTGGCACTGGAAGCCCTAGTA  
 CAGCTGCGTGGAAAGATTGACATCCAAGATTGGAGAGGGTTCATCTGATCGTGGCAGGTGG  
 TTATGACGAGAGAGTCCTGGAGAATGTGGAACATTATCAGGAATTGAAGAAAATGGTCCAAC  
 AGTCCGACCTGGCCAGTATGTGACCTTCTTGAGGTCTTCTCAGACAAACAGAAAATCTCC  
 CTCCTCCACAGCTGCACGTGTGCTTACACACCAAGCAATGAGCACTTGGCATTGTC  
 TCTGGAAAGCCATGTACATGCAGTGCCCAGTCATTGCTGTTAACATTGGGTGGACCCATTGGAGT  
 CCATTGACCACAGTGTACAGGGTTCTGTGAGCCTGACCCGGTGCACCTCTCAGAAGCA  
 ATAGAAAAGTCATCCGTAAACCTTCTAAAAGCCACCATGGGCTGGCTGGAAGAGCCAG  
 AGTGAAGGAAAATTTCCTGAAGCATTACAGAACAGCTCTACCGATATGTTACCAAAC  
 TGCTGGTA**TAA**TCAAGATTGTTTAAGATCTCCATTAATGTCATTGTTATGGATTGTAGACC  
 CAGTTTGAAACCAAAAAAGAAACCTAGAATCTAATGCAGAAGAGATCTTAAAAAATAAA  
 CTTGAGTCTTGAATGTGAGCCACTTCCTATATACCACACCTCCGTCCACTTCA  
 AACCATGTCTTATGCTATAATCATTCCAAATTGCCAGTGTAAAGTTACAAATGTGGTG  
 TCATTCCATGTTAGCAGAGTATTAAATTATATTCTCGGGATTATTGCTCTGTCTA  
 TAAATTGAAATGATACTGTGCCTTAATTGGTTTCAAGTTAAAGTGTGTATCATTCAA  
 AGTTGATTAATTGGCTTCAGTATAATGAGAGCAGGGCTATTGTAGTTCCAGATTCAA  
 CCACCGAAGTGTCACTGTCATCTGTTAGGAAATTGTTGTCCTGTCTTGCCTGGATC  
 CATAGCGAGAGTGCTCTGTATTGTTAAGATAATTGTATTGTCACACTGAGATATAA  
 TAAAAGGTGTTATCATAAAAAAAAAAAAAAA

## **FIGURE 116**

MPLLKLVHGSPLVGEKFKLFTLVSACIPVFRLLARRKKILFYCHFPDLLLTKRDSFLKRLY  
RAPIDWIEEYTTGMADCILVNSQFTAASFKETFKSLSHIDPDVLYPQLPSLNVTSDSVVPEKLD  
DLVPKGKKFLLSINRYERKKNLTLALEALVQLRGRLLTSQDWERVHLIVAGGYDERVLENVE  
HYQELKKMVQQSDLGQYVTFLRSFSDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMQCPV  
IAVNSGGPLESIDHSVTGFLCEPDPVHFSEAIKEFIREPSLKATMGLAGRARVKEKFSPEAF  
TEQLYRYVTKLLV

**Signal peptide:**

amino acids 1-15

**FIGURE 117**

GACTACGCCGATCCGAGACGTGGCTCCCTGGCGGCAGAACCAATGTTGGACTCGCGATCTT  
 CGCCGTTACCTTCTTGCCTGGCGTTGGTGGGAGCCGTGCTCACCTCTATCCGGCTTCAGAC  
 AAGCTGCAGGAATTCCAGGGATTACTCCAACGTAAAGAAAAAGATGGTAATCTTCCAGATATT  
 GTGAATAGTGGAAAGTTGCATGAGTTCTGGTTAATTGCATGAGAGATATGGGCCTGTGGT  
 CTCCTCTGGTTGGCAGGCCTCGTGGTTAGTTGGCAGTGTGATGTACTGAAGCAGC  
 ATATCAATCCAATAAGACATCGGACCCTTGAAACCATGCTGAAGTCATTATTAAGGTAT  
 CAATCTGGTGGTGGCAGTGTGAGTGAAAACCACATGAGGAAAAATTGTATGAAAATGGTGT  
 GACTGATTCTCTGAAGAGTAACTTGCCCTCCTCTAAAGCTTCAGAAGAATTATTAGATA  
 AATGGCTCTCCTACCCAGAGACCCAGCACGTGCCCTCAGCCAGCAGCATATGCTGGTTTGCT  
 ATGAAGTCTGTTACACAGATGGTAATGGTAGTACATTGAAGATGATCAGGAAGTCATTG  
 CTTCCAGAAGAACATGGCACAGTTGGTCTGAGATTGAAAAGGCTTCTAGATGGTCAC  
 TTGATAAAAACATGACTCGGAAAAACAATATGAAGATGCCCTCATGCAACTGGAGTCTGTT  
 TTAAGGAACATCATAAAAGAACGAAAAGGAAGGAACCTCAGTCAACATATTTCATTGACTC  
 CTTAGTACAAGGAAACCTTAATGACCAACAGATCCTAGAAGACAGTATGATATTTCTCTGG  
 CCAGTTGCATAATAACTGCAAAATTGTGTACCTGGCAATCTGTTTTAACACCTCTGAA  
 GAAGTTCAAAAAAAATTATATGAAGAGATAAACCAAGTTGGAAATGGTCTGTTACTCC  
 AGAGAAAATTGAGCAGCTCAGATATTGTCAGCATGTGCTTGTGAAACTGTTCGAACTGCCA  
 AACTGACTCCAGTTCTGCCAGCTCAAGATATTGAAGGAAAATTGACCGATTATTATT  
 CCTAGAGAGACCCCTCGTCCTTATGCCCTGGTGTGGTACTTCAGGATCCTAATACTGGCC  
 ATCTCCACACAAGTTGATCCAGATCGGTTGATGATGAATTAGTAATGAAAACCTTCT  
 CACTGGATTCTCAGGCACACAGGGAGTGTCCAGAGTTGAGGTTGCATATATGGTACCC  
 GTACTCTTAGTGTATTGGTAAGAGACTGCACCTACTTCTGTGGAGGGACAGGTTATTGA  
 AACAAAGTATGAACTGGTAACATCATCAAGGGAAAGAAGCTTGGATCACTGTCTCAAAGAGAT  
 ATTTAAAAATTATACATTAAAATCATTGTTAAATTGATTGAGGAAAACAACCATTAAAAA  
 AAATCTATGTTGAATCCTTTATAAACCAAGTATCAGTTGTAATATAAACACCTATTGTAC  
 TTAA

## **FIGURE 118**

MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGIPTEEKDGNDLPIVNSGSLHEFLVNLH  
ERYGPVVSFWFGRRLVVSLGTVDVLKQHINPNKTSDFETMLKSLLRYQSGGGSVSENHMRK  
KLYENGVTDSLKSNFALLKLSEELLDKWLSYPETQHVPLSQHMLGFAMKSVTQMVMGSTFE  
DDQEVIREFQKNHGTWSEIGKGFLDGSLDKNMTRKKQYEDALMQLESVLRNIKERKGRNFS  
QHIFIDSLVQGNLNDQQILEDSMIFSLASCIITAKLCTWAICFLTTSEEVQKKLYEEINQVF  
GNGPVTPEKIEQLRYCQHVL CETVRTAKLTPVSAQLQDIEGKIDRFIIIPRETLVLYALGVVL  
QDPNTWPSPHKFDPDRFDELVMKTFSSLGFSGTQECPELRFAYMVTIVLLSVLKRLHLLS  
VEGQVIETKYELVTSSREEAWITVSKRY

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 271-290

**FIGURE 119**

CTAGATTGTCGGCTTGCAGGGAGACTTCAGGAGTCGCTGTCTGAACCCAGCCTCAGA  
GACCGCCGCCCTGTCCCCGAGGGCC**ATG**GGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTC  
CTGACGCTCCTGGCGCATCTGGTGGTCGTACACCTTATTCTGGTCCCAGGACAGAACAT  
ACAGGCCTGCCTGCCTCACGTTCACCCCCGAGGAGTATGACAAGCAGGACATTAGCTGG  
TGGCCCGCTCTGTCAACCCTGGCCTCTTGCACTGGAGCTGGCCGGTTCCCTCAGGA  
GTCTCCATGTTAACAGCACCCAGAGCCTCATCTCCATTGGGCTCACTGTAGTGCATCCGT  
GGCCCTGTCTTCTCATATTGAGCGTTGGGAGTGCACTAGTATTGGTACATTTTGCT  
TCTGCAGTGCCTTCCAGCTGTCACTGAAATGGCTTATTGTCACCGTCTTGGGCTGAAA  
AAGAAACCCCTCT**TGA**TTACCTTCATGACGGAACCTAAGGACGAAGCCTACAGGGCAAGGG  
CCGCTTCGTATTCTGGAAAGAAGGAAGGCATAGGCTCGGTTCCCTCGGAAACTGCTTC  
TGCTGGAGGATATGTGTTGAAATAATTACGTCTTGAGTCTGGGATTATCCGCATTGTATTTA  
GTGCTTGTAATAAAATGTTGTAGTAACATTAAGACTTATACAGTTAGGGACA  
ATTAAAAAAA

## **FIGURE 120**

MGRVSGLVPSRFLTLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLG  
LFAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCSALPAVT  
EMALFVTVFGLKKKPF

### **Transmembrane domain:**

amino acids 12-28 (type II), 51-66, 107-124

**FIGURE 121**

TCCCGGACCCTGCCGCCCTGCCACTATGTCCC GCCGCTCTATGCTGCTTGCCTGGGCTCTCC  
CCAGCCTCCTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCCTGCTGCAGCCCCATA  
GTGCCCGGAACGAGTGGAAAGGCCCTGGCATCAGAGTGCAGCCCAGCACCTGAGCCTGCCCTT  
ACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGCTGCAACACCCCCGCCTCGTGCCAGC  
AGCAGGCCCGGAATGTGCAGCACTACCACATGAAGACACTGGGCTGGTGCACGTGGCTAC  
AACTCCTGATTGGAGAACGAGACGGCTCGTATACGAGGGCCGTGGCTGGAACTTCACGGGTGC  
CCACTCAGGTCACTTATGGAACCCATGTCCATTGGCATCAGCTTATGGCAACTACATGG  
ATCGGGTGCCACACCCAGGCCATCCGGGCAGCCCAGGGTCTACTGGCCTGCGGTGTGGCT  
CAGGGAGCCCTGAGGTCCAATATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTC  
TCCAGGCAACCAGCTTACCAACCTCATCCAGAATTGCCACACTACCGCTCCCCTGAGGCC  
CTGCTGATCCGCACCCATTCCCTCCCATGCCAAAAACCCCACTGTCTCCTTCTCCA  
ATAAAGATGTAGCTC

## **FIGURE 122**

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT  
AGSSCNTPASCQQQARNVQHYHMKTGCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP  
MSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL  
IQNWPHYRSP

**Signal peptide:**

amino acids 1-20

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20

## **FIGURE 123**

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAAG**ATG**CACT  
 GACTCGCTGCTCGTGTCTGGTCAGGGTAGCCTATCTGGTCATCTGTGGCCAGG  
 ATGATGGTCCTCCCAGGCTCAGAGGACCCGTGACGCTGATGACCACGAGGGCCAGCCCCGGCCC  
 CGGGTGCCTCGGAAGCGGGGCCACATCTCACCTAACGTCAGGCCCCATGGCCAATTCCACTCT  
 CCTAGGGCTGCTGGCCCCGCCTGGGGAGGCTTGGGCATTCTTGGCAGCCCCCAACGCC  
 CGAACACAGCCCCCACCCCTCAGCCAAGGTGAAGAAAATCTTGGCTGGGCAGTTCTAC  
 TCCAACATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGGAAAGATTGTGGACCATGGCAA  
 TGGGACCTTCAGCGTCCACTTCAAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCC  
 TCGTCCCCCCCAGTAAAGCTGTAGAGTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAG  
 GCCTCCAAAATCTTCAACTGCCGGATGGAGTGGGAGAAGGTAGAACGGGCCGCGACCTC  
 GCTTGCACCCACGACCCAGCCAAGATCTGCTCCGAGACCACGCTCAGAGCTCAGCCACCT  
 GGAGCTGCTCCAGCCCTCAAAGTCGTCTGTCTACATGCCCTTACAGCACGGACTAT  
 CGGCTGGTCCAGAAGGTGTGCCAGATTACAACCTACCATAGTGATAACCCCTACTACCCATC  
 TGGG**TGA**CCCGGGGCAGGCCACAGAGGCCAGGCCAGGGCTGGAAGGACAGGCCCTGCCCATGC  
 AGGAGACCATCTGGACACCAGGGCAGGGAAAGGGGTGGGCCTCAGGCAGGGAGGGGGTGGAG  
 ACGAGGAGATGCCAAGTGGGCCAGGGCCAAGTCTCAAGTGGCAGAGAAAGGGTCCAAGTG  
 CTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGGAGGAGGAGTGGCT  
 CTCTGTGCAGCCTCACAGGGCTTGCACGGCACAGAGAGATGCTGGTCCCCGAGGCC  
 TGTGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGAGGAAGCTAACGCCCTGGTT  
 CTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGAGATTTCATCAGTGTGGACAGCCTG  
 TCAACTTAGGATGGATGGCTGAGAGGGCTCCTAGGAGGCCAGTCAGCAGGGTGGGTGGGC  
 CAGAGGAGCTCCAGCCCTGCCTAGTGGCGCCCTGAGCCCTTGTGCTGCTGAGCATG  
 GCATGAGGCTGAAGTGGCAACCCCTGGGTCTTGATGTCTTGACAGATTGACCATCTGTCTC  
 CAGCCAGGCCACCCCTTCCAAAATTCCCTTCTGCCAGTACTCCCCCTGTACCAACCCATT  
 GCTGATGGCACACCCATCCTTAAGCTAACAGACAGGACGATTGTGGCTCCACACTAACGCC  
 ACAGCCCACCCATCCCGTGTGTGTCCCTCTCCACCCCAACCCCTGCTGGCTCCTCTGGAG  
 CATCCATGTCCCGAGAGGGGTCCCTAACAGTCAGCCTCACCTGTACGACACCAGGGTTCTCC  
 CGGATCTGGATGGCGCCGCTCTCAGCAGCGGGCACGGGTGGGCGGGGCCGGCGCAGA  
 GCATGTGCTGGATCTGTTCTGTGTCTGTGCTGTGGGTGGGGAGGGGAGGGAAAGTCTGT  
 GAAACCGCTGATTGCTGACTTTGTGTGAAGAATCGTGTCTGGAGCAGGAATAAGCTT  
 GCCCCGGGGCA

## **FIGURE 124**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521
><subunit 1 of 1, 252 aa, 1 stop
><MW: 28127, pI: 8.91, NX(S/T): 5
MQLTRCCFVFLVQGSLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMAN
STLLGLLAPPGEAWGILGQPPNRPNHSPPSAKVKKIFGWGDFYSNIKTVVALNLLVTGKIVD
HGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMEWEKVERGR
RTSLCTHDPAKICSRDHAQSSATWSCSQPKVVCVYIAFYSTDYRLVQKCPDNYHSDTPY
YPSG
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-14

**N-glycosylation sites.**

amino acids 62-65, 127-130, 137-140, 143-146

**2-oxo acid dehydrogenases acyltransferase**

amino acids 61-71

## **FIGURE 125**

GTGAATGTGAGGGTTGATGACTTCAGATGTCTAGGAACCAGAGTGGTGCAGGGCCCCA  
 GGCAGGGCTGATTCTGGCGGAGGAGAGTAGGGTAAAGGGTCTGCATGAGCTCCTAAAG  
 GACAAAGGTAAACAGAGCCAGCGAGAGAGCTCGAGGGGAGACTTGACTTCAAGCCACAGAAT  
 TGGTGGAAAGTGTGCGGCCGCGCCGCGCTCGCTCCTGCAGCGCTGTCGACCTAGCCGCTAG  
 CATCTTCCCAGCACCGGGATCCGGGTAGGAGGCGACGCCGGCGAGCACCAAGGCCAGCC  
 GGCTGCGGCTGCCACACGGCTCACC**ATGG**GCTCCGGCGCCGGCGCTGTCGCCGGTGC  
 GCCGTGCTGCTGGTCCTCACGCTGCCGGGCTGCCGTCTGGCACAGAACGACACGGAGCC  
 CATCGTGCCTGGAGGGCAAGTGTCTGGTGGTGCAGTCGAACCCGCCACGGACTCCAAGG  
 GCTCCTCTCCTCCCCGCTGGGATATCGGTCCGGCGGCCACTCCAAGGTGCCCTCTCG  
 GCGGTGCGGAGCACCAACCACGAGCCATCCGAGATGAGCAACAAGACGCGCATATTTACTT  
 CGATCAGATCCTGGTGAATGTGGTAATTTTACATTGGAGTCTGTCTTTAGCACCAA  
 GAAAAGGAATTACAGTTCAAGTTCAAGTAAAGTCTACCAGAGCCAAACTATCCAG  
 GTTAACTTGATGTTAAATGGAAAACCAGTAATATCTGCCTTGCAGGGGACAAAGATGTTAC  
 TCGTGAAGCTGCCACGAATGGTGCCTGCTCACCTAGATAAAAGAGGATAAGGTTACCTAA  
 AACTGGAGAAAGGTAAATTGGTGGAGGCTGGCAGTATTCCACGTTCTGGCTTCTGGT  
 TTCCCCCTA**TAG**GATTCAATTCTCCATGATGTTCATCCAGGTGAGGGATGACCCACTCCTG  
 AGTTATTGGAAGATCATTTCATCATTGGATTGATGTCTTTATTGGTTCTCATGGGTG  
 GATATGGATTCTAAGGATTCTAGCCTGTCGAACCAATAACAAATTACAGATTATTGTG  
 TGTGCTGTTCAAGTATTTGGATTGGACTCTAACGAGATAAACCTATGCTAAATGTA  
 ACAGTCAAAAGCTGCTGCAAGACTTATTCTGAATTTCATTCTGGATTACTGAATTAGT  
 TACAGATGTGAAATTATTGTTAGTTAAAGACTGGCAACCAGGTCTAAGGATTAGA  
 AAAACTCTAAAGTTCTGACTTCAATCAACGGTTAGTGTGATACTGCCAAAGAACTGTATACTG  
 TGTTAATATATTGATTATTTGTTTATTCCCTTGAATTAGTTGTTGGTTCTGTAA  
 AAAACTGGATTTTTCAGTAACTGGTATTATGTTCTCTAAAATAAGGTAATGAA  
 TGGCTGCCACAAATTACCTGACTACGATATCATGACATGACTCTCTCAAAAAAAA  
 GAATGCTCATAGTTGTATTTAATTGTATATGTGAAAGAGTCATATTTCCAAGTTATATT  
 TTCTAAGAAGAAGAATAGATCATAATCTGACAAGGAAAAGTTGCTTACCCAAATCTAAG  
 TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCGAGGGAAATCTTATACTTTATTG  
 TCAACTTAAATTAAATGATTGATAATAACCACCTTATTAAAAACCTAAGGTTTTTT  
 TCCGTAGACATGACCACTTTATTAAACTGGTGGGATGCTGTTCTAATTATACCTAT  
 TTTCAAGGCTCTGTTGATTGAAAGTATCATCTGGTTGCCTTAACCTTAAATTGTA  
 TATATTATCTGTTAGCTAATATTAAATTCAAATATCCCATATCTAAATTAGTGC  
 ATATTCTGCTTTGTATAGGTCAATGAAATTCAAAATTATTATGCTGTTAGAATAAAGA  
 TTAATATATGTTAAAAAAA

## **FIGURE 126**

MGSRRALSAVPAVLLVLTLPGLPVWAQNDTEPIVLEGKCLVVCDSPATDSKGSSSPLGI  
SVRAANSKVAFAVRSTNHEPSEMSNKTRIIFYFDQILVNVGNNFTLESVFVAPRKGIYSFSF  
HVIKVYQSQTIQVNMLNLNGKPVISAFAAGDKDVTREAATNGVLLYLDKEDKVYLKLEKGNLVG  
GWQYSTFSGFLVFPL

**Signal peptide:**

amino acids 1-27

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**FIGURE 127**

CGGTGGCC**ATG**ACTGC~~GGCC~~GTGTTCTCGGCTGCGC~~TT~~CATTGCC~~TT~~CGGGC~~CT~~GCGCTC  
GCC~~CTT~~TATGTCTTCACC~~AT~~CGGCC~~AT~~CGAGCC~~GT~~GC~~GT~~ATCATCTC~~CT~~CATGCC~~GG~~GAC  
TTTCTTCTGGTTGGTGTCTACTGATT~~TC~~GTCC~~CT~~TGTTGGTT~~CAT~~GGCAAGAGTC~~ATTA~~  
TTGACAACAAAGATGGACCAACACAGAAATATCTGCTGATCTTGAGC~~GTT~~GTCTGTC  
TATATCCAAGAAATGTTCCGATTGCATATTATAAACTCTTAAAAAAAGCCAGTGAAGGTT  
GAAGAGTATAAACCCAGGTGAGACAGCACCC~~CT~~TATGCGACTGCTGCC~~CT~~TGTTCTGGCT  
TGGGCTT~~GG~~AATCATGAGTGGAGTATT~~TC~~CTTGTGAATACC~~CT~~TACTGACTC~~CT~~TGGGG  
CCAGGCACAGTGGGCATT~~AT~~CATGGAGATT~~TC~~C~~CT~~CAATT~~TC~~C~~TT~~ATT~~CAG~~CTTCATGAC  
GCTGGTCATTATCTGCTGCATGTATTCTGGGGCATTGTATTTTGATGGCTGTGAGAAGA  
AAAAGTGGGCATC~~CT~~C~~TT~~TATCGTTCTC~~CT~~GACCCACCTGCTGGTGT~~CAG~~CCCAGACCTTC  
ATAAGTTCTTATTATGGAATAAACCTGGCGTCAGCATTATAATCCTGGTGCTCATGGGCAC  
CTGGGCATTCTTAGCTGC~~GGG~~AGGCAGCTGCC~~GA~~AGC~~CT~~GAAACTCTGCCTGCTCTGCCAAG  
ACAAGAAC~~TT~~CTT~~CT~~TTACAACCAGCGCTCCAGA**TAA**CC~~TC~~AGGGACCAGCA~~CT~~CCCCAA  
ACCGCAGACTACATCTTAGAGGAAGCACA~~ACT~~GTGC~~CT~~TTTCTGAAAATCC~~CT~~TTTCTG  
GTGGAATTGAGAAAGAAATAAAACTATGCAGATA

## **FIGURE 128**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658
><subunit 1 of 1, 257 aa, 1 stop
><MW: 28472, pI: 9.33, NX(S/T): 0
MTAAVFFGCAFIAFGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDN
KDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGF
GIMSGVFSFVNTLSLPGTVGIHGDSPQFFLYSAFMTLVIIILLHVFWGIVFFDGCEKKW
GILLIVLLTHLLVSAQTFISSLYYGINLASAFIILVLMGTWAFLAAGGSCRSLKLCLLCQDKN
FLLYNQRSR
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domains:**

amino acids 32-51, 119-138, 152-169, 216-235

**Glycosaminoglycan attachment site.**

amino acids 120-123

**Sodium:neurotransmitter symporter family protein**

amino acids 31-65

## FIGURE 129

CGGCAACCAGCCGCCACCACCGCTGCCACTGCCGCCCTGCCGGGGCC**ATGTTCGCTCTGGGCTTGCCCTTCT**  
 TGGTGCCTTGGCCTCGGTGAGAGCCATCTGGGGTTCTGGGGCCAAGAACGTCAGCAGAAAGACGCC  
 AGTTTGAAGCGCACCTACGTGGACGAGGTCAACACGGAGCTGGTAACATCTACACCTCAACCATACTGTGACCC  
 GCAACAGGACAGAGGGCGTGTGTGAAACAGCAGAAGGGCGCCGTTGCTGTTGTGG  
 TCCGCCAGAAGGAGGCTGTGTGTCCTCCAGGTGCCCCTAATCTGCGAGGGATGTTCAGCGCAAGTACCTCT  
 ACCAAAAAGTGGAACGAACCTGTGTCAAGCCCCCACCAGAAAGATGAGTCGGAGATTCAAGTCTTCTACGTGGATG  
 TGTCCACCCGTCAACAGTCACACACCATAACAGCTCCGGTCAGCCCATGGACGATTTGTGCTCAGGACTG  
 GGGAGCAGTTCAAGCTTCAATACACAGCAGCACAGCCCCAGTACTTCAGTATGAGTTCAGGCTGAAGGCGTGGACT  
 CGGTAATTGTCAAGGTGACCTCCAACAAGGCTTCCCTGCTCAGTCATCTCCATTCAAGGATGTGCTGTGCTG  
 TCTATGACCTGGACAACAACGTTAGCCTCATCGGCATGTACAGACGATGACCAAGAAGGCGGCATCACCGTAC  
 AGCGCAAAGACTTCCCCAGCAACAGCTTTATGTGGTGGTGGTGAAGACCGAAGACCAAGCCTGCCGGGCT  
 CCCTGCCCTTCTACCCCTCGAGAAGATGAACGGCTGATCAAGGGCACCGCCAGAAAACCTGTCAAGTGGCTGG  
 TGTCTCAAGCAGTCACGTCTGAGGCATACGTCACTGGATGCTCTTGCCTGGTATATTCTCTCTTTTAC  
 TGCTGACCGTCCCTCCGTGCTGGAGAACTGGAGGCAGAAGAAGAACCCCTGCTGGTGGCCATTGACCGAG  
 CCTGCCAGAAGCGGTACCCCTGAGCTGGCTGATTCTTCCTGGCAGTCCCTTATGAGGGTTACAAC  
 ATGGCTCTTGAGAATGTTCTGGATCTACCGATGGTCTGGTGAACAGCGCTGGCACTGGGACCTCTTAC  
 GTTACCAAGGGCCGCTCTTGAAACCTGTAGGTACTCGGCCCCAGTGGACTCCATGAGCTCTGTGGAGGGATG  
 ACTACGACACATTGACCGACATCGATTCCGACAAGAATGTCATTGCAACAGCAAACTCTATGTGGCTGACC  
 TGGCACCGAAGGACAAGCGTGTCTGCGGAAAAGTACCAAGATCTACTTCTGGAACATTGCCACATTGCTGTCT  
 TCTATGCCCTTCTGTGGTGCAGCTGGTACCTACAGACGGTGGTGAATGTCACAGGAATCAGGACATCT  
 GCTACTACAACCTTCTCTGCCACCCACTGGCAATCTCAGCGCTTCAACAAACATCCTCAGCAACCTGGGT  
 ACATCCTGCTGGGCTGCTTTCTGCTCATCATCTGCAACGGAGATCAACCAACACCGGGCTGCTGCGCA  
 ATGACCTCTGCGCTGGAATGTGGGATCCCCAACACTTGGGCTTCTACGCCATGGCACAGCCCTGATGA  
 TGGAGGGCTGCTAGTGTCTATCATGTGTGCCAACACTAACAAATTCCAGTTGACACATCGTTCATGT  
 ACATGATGCCGAACTCTGATGTAAGCTTACCAAGCAGGGCACCCGACATCAACGCCAGCGCTACAGTG  
 CCTACGCCCTGCCCTGGCAATTGTCATCTCTCTGTGCTGGCGTGGCTTGGCAAAGGGAACACGGCTTCT  
 GGATGCTCTCTCCATTCACATCATGCCACCCCTGCTCAGCACGAGCTCTATTACATGGCCGGTGG  
 AACTGGACTCGGGATCTCCGCCGCATCCTCACGTGCTACAGACTGCATCCGGCAGTGCAGCGGGCC  
 TCTACGTGGACCGCATGGTGTGCTGGTACGGCAACGTCACTGGTCAGCTGGCTGCCTATGGCTTATCA  
 TGCGCCCAATGATTGCTCTACTTGTGGCATTGGCATCTGCAACCTGCTCTTACTTCGCTTCTACA  
 TCATCATGAAGCTCCGGAGTGGGAGAGGATCAAGCTCATCCCCCTGCTCTGCATGTTGCACCTCCGGTCT  
 GGGGCTCGCGCTTCTCTCCAGGACTCAGCACCTGGCAGAAAACCCCTGAGAGTCGAGGGAGCACA  
 ACCGGGACTGCATCCTCGACTTCTTGACGACCACGACATCTGCACCTCCCTCCATGCCATGTTG  
 GGTCTCTGGTGTGCTGACACTGGATGACGACCTGGATACTGTGAGCAGGGACAAGATCTATGTCCT**TAGC**  
 AGGAGCTGGGCCCTCGCTCACCTCAAGGGCCCTGAGCTCTTGTGTCATAGACCGGTACTCTGCTGCT  
 GTGGGAGTAGTCCCAGCACCGCTGCCAGCAGTGGATGGCAGCAGGACAGCCAGGTCTAGCTTAGGCTGGCCT  
 GGGACGCCATGGGCTGGCATGGAACCTGCAAGCTGCCCTGAGGAGCAGGCCGCTGCTCCCTGGAAACCCCC  
 AGATGTTGGCAAATTGCTGTTCTCTCAGTGTGGGCTTCCATGGGCCCTGCTCTTGGCTCTCCATT  
 GTCCCTTGCAAGAGGAAGGAGTGGAAAGGGACACCCCTCCCCATTTCATGCCCTGCAATTGCCCCCTCTCCCC  
 ACAATGCCCAAGCCTGGACCTAAAGGCCCTTCTCTCCCATACTCCCACTCCAGGGCTAGTCTGGGGCCTGA  
 ATCTGTCCTGATCAGGGCCCAGTTCTCTTGGCTGCTGCCATCAGTCCCTGCCATCAGGCCATTCCAGTCAGCC  
 AGGATGGATGGGGTATGAGATTGTTGGGTTGGCCAGCTGGCAGACATTGGTCAAGGCCCTGCAAGGGG  
 CCTGGGGCAGTGCCTATTCTCTCCCTGACCTGTGCTCAGGGCTGGCTTCTAGAAAGGGCTTCAGGAAGGGATGTGCTGTT  
 TGAGAACCGCCTCTGATTCAAGAGGCTGAATTCAAGGGCTCACCTCTTCATCCCATCAGCTCCAGACTGATGCC  
 AGCACCAAGACTGGAGGGAGAAGCGCCTCACCCCTCCCTCTTCCAGGCCCTTAGTCTGCAAACCCCC  
 AGCTGGTGGCCTTCAGTGCACACTGCCAAGAATGTCAGGGCAAGGGAGGATGATAACAGAGTTAG  
 CCCGTTCTGCCCTCACAGCTGTGGCACCCAGTGCCTACCTAGAAAGGGCTTCAGGAAGGGATGTGCTGTT  
 CCCTCTACGTGCCCTAGCCTCGCTCTAGGACCCAGGGCTGGCTCTAAGTTCCGTCAGTCAGGCC  
 AGTTCTGTTAGTCATGCACACACATACCTATGAAACCTTGAGTTACAAGAATTGCCCAAGCTGGGCAC  
 CCTGGCACCCCTGGCCTTGGATCCCCTCGTCCCACCTGGCCACCCAGATGCTGAGGATGGGGAGCTCAGG  
 CGGGGCTCTGCTTTGGGATGGAATGTTCTCCCAAACCTGTTTATAGCTGCTGTTGAAGGGCTGG  
 AGATGAGGTGGGCTGGATCTTTCTCAGAGCGTCCATGCTATGGTGCATTCCGTTCTATGAATGAATT  
 TGCATTCAATAAACACCAGACTCAAAAAAAAAAA

**FIGURE 130**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659
><subunit 1 of 1, 832 aa, 1 stop
><MW: 94454, pI: 6.94, NX(S/T): 12
MFALGLPFLVLLVASVESHLGVLPKNVSQKDAEFERTYVDEVNSELVNIYTFNHTVTRNRT
EGVRVSVNVLNKQKGAPLLFVVRQKEAVVSFQVPLILRGMFQRKYLYQKVERTLCQPPTKNE
SEIQFFYVDVSTLSPVNNTYQLRVSRMDDFVLRTGEQFSFNTTAAQPQYFKYEFP EGVD SVI
VKVTSNKA FPCSVISI QDVLCPVYDLDNNVA FIGMYQTMTKKA ITVQRKDFPSNSFYVVVV
VKTEDQACGGSLPFYPFAEDEPV DQGHRQKTL S VL VSQAVTSEAYVSGMLFCLGIFLSFYLL
TVLLACWENWRQKKKTLLVAIDRACPESGHPRV LADSFPGSSPYEGYN YGSFENVSGSTDGL
VDSAGTGDL SYGYQGRSFE PVGTRPRV DSMSSVE EDDYDT LTDIDSDKNVIRTKQYLYVADL
ARKDKRVLRK KYQIYFWNIATIAF YALPVVQLVITYQ TVVNVTGNQDICYYNFLCAHPLGN
LSAFNNILSNLGYILLG LLFLLI ILQREINHN RALLRN DLCALECGIPKH FGLFYAMGTALM
MEGLLSACYHVC PNYTNFQFDTSF MYMIAGLCMLKLYQKRHPDINASAYSAYACLAIVIFFS
VLGVVFGKGNTAFWIVFSIIHI IATLLL STQLYYMGRWKLD SGIFRRILHVLYTDCIRQCSG
PLYVDRMVLLVMGNVINWSLAAYGLIMRPND FASYLLAIGICNLLYFAFYIIMKLRSGERI
KLIPLL CIVCTSVVWGFA LFFFQGLSTWQKTPAESREHN RDCILLDFDDHDIWHF LSSIA
MFGSFLVLLTLDDDTVQRDKIYVF
```

**Important features of the protein:****Signal peptide:**

amino acids 1-18

**Transmembrane domains:**

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

**Leucine zipper pattern.**

amino acids 497-518

**N-glycosylation sites.**

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

## **FIGURE 131**

GCTCAAGTGCCTGCCCTGCCACCCAGCCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC  
 TCTCTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGCCTGGAGGGCTGTCCTG  
**ACCATG**TCCCTGCCTGGCTGTGGCTGCTTGTCTCCGCCCCAGGCTCTCCCAAGGC  
 CCAGCCTGCAGAGCTGTGAGTTCCAGAAAATATGGTGGAAATTCCCTTATACC  
 TGACCAAGTTGCCCTGCCCGTGAGGGGCTGAAGGCCAGATCGTGCCTGAGGGACTCA  
 GGCAAGGCAACTGAGGCCATTGCTATGGATCAGATTCTGGCTTCTGCTGGTACCCAG  
 GCCCTGGACCGAGAGGAGCAGGCAGAGTACCGACTACAGGTACCCCTGGAGATGCAGGATG  
 GACATGTCTTGTGGGTCCACAGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAGGTG  
 CCCCCATTCTCAAGCCATCTACAGAGCTCGGCTGAGCCGGGTACCAAGGCCTGGCATCCC  
 CTTCCCTTCTGAGGCTTCAGACCGGGATGAGCCAGGCACAGCCAACCTGGATCTCGAT  
 TCCACATCCTGAGCCAGGCTCCAGCCCAGCCTCCCCAGACATGTTCCAGCTGGAGCCTCGG  
 CTGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACCAGCCTGACCACGCCCTGGAGAGGAC  
 CTACCAAGCTGTTGGTACAGGTCAAGGACATGGTGACCAGGCCTCAGGCCACCAGGCCACTG  
 CCACCGTGAAGTCTCCATCATAGAGGACCTGGGTGTCCTAGAGCCTATCCACCTGGCA  
 GAGAATCTCAAAGTCTATAACCGCACCATGGCCAGGTACACTGGAGTGGGGTGTGATGT  
 GCACTATCACCTGGAGAGCCATCCCCGGGACCTTGAAGTGAATGAGCAGAGGGAAACCTCT  
 ACGTGACCAGAGAGCTGGACAGAGAACGCCAGGCTGAGTACCTGCTCCAGGTGCGGGCTCAG  
 AATTCCCATGGCGAGGACTATGCGGCCCTCTGGAGCTGCACGTGCTGGTATGGATGAGAA  
 TGACAACGTGCCTATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCTCAGTCCAC  
 CAGGTACTGAAGTGAAGTAGACTGTCAAGCAGAGGATGCAGATGCCCGGCTCCCCAATTCC  
 CACGTTGTGATCAGCTCTGAGCCCTGAGCCTGAGGATGGGTAGAGGGAGAGCCTTCCA  
 GGTGGACCCCACCTCAGGCAGTGTGACGCTGGGGTGCCTCCACTCCAGCAGGCCAGAAC  
 TCCTGCTTCTGGTGCCTGGCATGGACCTGGCAGGGCGCAGAGGGTGGCTTCAGCAGCACGTG  
 GAAGTCGAAGTCGCACTGACAGATATCAATGATCACGCCCTGAGTTCATCACTCCAGAT  
 TGGGCCTATAAGCCTCCCTGAGGATGTGGAGCCGGGACTCTGGTGGCCATGCTAACAGCCA  
 TTGATGCTGACCTCGAGCCGCCCTCCGCTCATGGATTTGCCATTGAGAGGGAGACACA  
 GAAGGGACTTTGGCCTGGATTGGGAGCCAGACTCTGGCATGTTAGACTCAGACTCTGCAA  
 GAACCTCAGTTATGAGGCAGCTCAAAGTCATGAGGTGGTGGTGCAGAGTGTGGCGA  
 AGCTGGTGGGGCCAGGCCAGGCCCTGGAGCCACGCCACGGTGACTGTGCTAGTGGAGAGA  
 GTGATGCCACCCCCCAAGTTGGACCAAGGAGAGCTACGAGGCCAGTGTCCCCATCAGTCCCC  
 AGCCGGCTTTCCGTGACCATCCAGCCCTCCGACCCATCAGCCGAACCTCAGGTTCT  
 CCCTAGTCATGACTCAGAGGGCTGGCTCTGCATTGAGAAATTCTCCGGGAGGTGCACACC  
 GCCCAGTCCCTGCAGGGGCCAGCCTGGGACACCTACACGGTGCTGTGGAGGCCAGGA  
 TACAGCCCTGACTCTGCCCTGTGCCCTCCCAATACCTCTGCACACCCCCGCAAGACCATG  
 GCTTGATCGTGAGTGGACCCAGCAAGGACCCGATCTGGCCAGTGGCACGGTCCCTACAGC  
 TTCACCCCTGGTCCAACCCACGGTGCAACGGGATTGGCCTCCAGACTCTCAATGGTTC  
 CCATGCCCTACCTCACCTGGCCCTGCATTGGTGAGCCACGTGAACACATAATCCCCGTGG  
 TGGTCAGCCACATGCCAGATGTGGCAGCTCTGGTGCAGTGATCGTGTGCTGCAAC  
 GTGGAGGGCAGTGCATGCGCAAGGTGGCCGCATGAAGGGCATGCCACGAAGCTGCGC  
 AGTGGGCATCCTGTAGGCACCCGGTAGCAATAGGAATCTCCTCATCCTCATTTCACCC  
 ACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTCCCCCTGAAGGCG  
 ACTGTCTGAATGGCCCAGGCAGCTAGCTGGAGCTTGGCCTCTGGCTCCATCTGAGTCCC  
 CTGGGAGAGAGCCCAGCACCCAAAGATCCAGCAGGGGACAGGACAGAGTAGAAGCCCCTCCAT  
 CTGCCCTGGGGTGGAGGCACCATCACCACCAACGGCATGTGAGCAGGCCATGGACACCAAC  
 TTTATGGACTGCCATGGGAGTGTCCAATGTCAGGGTGTGCCCCAATAATAAGCCCCA  
 GAGAACTGGCCTGGCCCTATGGGAAAAAAAAAAAAAAAG

**FIGURE 132**

MVPAWLWLLCVSVPQALPKAQPAELSVEVPENYGGNFPFLYLTKLPLPREGAEGQIVLSGDSG  
KATEGPFAMDPDSGFLLVTRALDREEQAELYQLQVTLEMQDGHLWGPQPVLVHVKDENDQVP  
HFSQAIYRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAPAQPSPDMFQLEPRL  
GALALSPKGSTSLDHALERTYQLLVQVKDMGDQASGHQATATVEVSIIESTWVSLEPIHLAE  
NLKVLYPHHMAQVHWSSGDVHYHLESHPPGPFEVNAEGNLYVTRELDRDREAQAEYLLQVRAQN  
SHGEDYAAPPLEHLVLMMDENDNVPICPPRDPTVSIPELSPPGTEVTRLSAEDADAPGSPNSH  
VVYQLLSPEPEDGVGRAFQVDPTSGSVTLGVPLRAGQNILLVIALMDLAGAEGGFSSSTCE  
VEVAVTDINDHAPEFITSQIGPISLPEDVEPGTLVAMLTAIDADLEPAFRIMDFAIERGDTE  
GTFGLDWEPDGHVRLRLCKNLSYEAPSHEVVVVVQSVAKLVGPGPGATATTVLVERV  
MPPPQKLDQESYEASVPISAPAGSFLLTIQPSDPISRTLRFSLVNDSEGWLICIEKFSGEVHTA  
QSLQGAQPGDTYTVLVEAQDTALTLPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF  
TLGPNPTVQRDWRLQTLNGSHAYLTLALHWVEPREHIIPVVVSHNAQMWMQLLVRVIVCRCNV  
EGQCMRKVGRMKGMPTKLSAVGILVGTVAIGIFLILIFTHWTMSRKDPDQPADSVPLKATV

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 762-784

## **FIGURE 133**

CCGGGGAC**ATG**AGGTGGATACTGTTCATGGGCCCTATTGGTCCAGCATCTGTGCCAA  
 GAAAAATTGGGACCAAGTTTGAGGATTAATGTCAGAAATGGAGACGAGATCAGCAA  
 ATTGAGTCAACTAGTGAATTCAAACAATTGAGCTCAATTCTGAAATCTCCCTCCCT  
 TCAATCGGCCTGTGGATGTCCTGGTCCATCTGTCAGTCTGCAGGCATTAAATCCTCCTG  
 AGATCCCAGGGCTTAGAGTACGCAGTGACAATTGAGGACCTGCAGGCCCTTAGACAATGA  
 AGATGATGAAATGCAACACAATGAAGGCCAAGAACGGAGCAGTAATAACTCAACTACGGGG  
 CTTACCATTCCCTGGAAGCTATTACACGAGATGGACAACATTGCCAGACTTCCTGAC  
 CTGGCGAGGAGGGTGAAGATTGGACATTGTTGAAAACCGGCCGATGTATGACTGAAGTT  
 CAGCACTGGGAAAGCGTGGCGCCGGCTTGGCTGAATGCAGGCATCCATTCCGAG  
 AGTGGATCTCCAGGCCACTGCAATCTGGACGGCAAGGAAGATTGTATCTGATTACCAAGGG  
 GATCCAGCTATCACCTCCATCTGGAGAAAATGGATATTTCTTGTGCGCTGCCCCAATCC  
 TGATGGATATGTGTATACTCAAACCTCAAACCGATTATGGAGGAAGACGCCGCCCCAAATC  
 CTGGAAAGCTCCTGCATTGGTGCCTGACCCAAATAGAAACTGGAACGCTAGTTTGAGGAAAG  
 GGAGCCAGCGACAACCCCTGCTCCGAAGTGTACCATGGACCCCACGCCAATTGGAAGTGG  
 GGTGAAATCAGTGGTAGATTCCAAAACATGGGAAATTCAAGGGCTTCATGACACTGC  
 ACAGCTACTCGCAGCTGCTGATGTATCCATATGGGTAACAGTCAAAAGGCCAGATGCC  
 GAGGAACCTGACAAGTGGCGAGGCTGGCCAAAGCTCTGGCTCTGTGTCGGGCACTGA  
 GTACCAAGTGGGCTCCACCTGCACCACTGTCTATCCAGCTAGCGGGAGCAGCATCGACTGG  
 CGTATGACAACGGCATCAAATTGCAATTGAGTTGAGAGATACCGGGACCTATGGC  
 TTCCTCCTGCCAGCTAACAGATCATCCCCACTGCAGAGGAGACGTGGCTGGGCTGAAGAC  
 CATCATGGAGCATGTGCGGGACAACCTCTAC**TAG**GCATGGCTCTGCTCTGTCTACATTAT  
 TTGTACCCACACGTGCACGCACTGAGGCCATTGTTAAAGGAGCTTTCCACCTGTGAG  
 TCAGAGCCCTGGGTTGTGGAGCACACAGGCCTGCCCTCTCCAGCCAGCTCCCTGGAGT  
 CGTGTGCTGGCGGTGCTGCAGAAGACTGGTCTGCCAGCCTGCTCAATTGGCCTG  
 CTGTTTTGATGAGCCTTGTCTGTTCTCCACCCCTGCTGGCTGGGCGGTGCACTC  
 AGCATCACCCCTCCTGGGTTGGCATGTCTCTACCTCATTAGAACCAAAGAACATC  
 TGAGATGATTCTCTACCCCATCCACATCTAGCCAAGCCAGTGACCTGCTCTGGGCACT  
 GTGGGAGACACCACTTGTCTTAGGTGGCTCAAAGATGATGTAGAATTCCCTTAATTTC  
 TCGCAGTCTCCTGGAAAATATTCCCTTGAGCAGCAAATCTGTAGGGATATCAGTGAAG  
 GTCTCCCTCCCTCCTGTTTTTTGAGACAGAGTTTGCTCTGGC  
 CAGGCTGGAGTGTGATGGCTCGATCTGGCTACCACAAACCTCTGCCCTGGGTTCAAGCA  
 ATTCTCCTGCCCTGCCTCAGCCTCTGGAGTAGCTGGTTATAGGCGCATGCCACCATGCCCTGGCTA  
 ATTTGTGTTTTAGTAGAGACAGGGTTCTCCATGTTGGTCAGGCTGGCTCAAACCTCCA  
 ACCTCAGGTGATCTGCCCTGGCCTCCAGAGTGTGGATTACAGGTGTGAGCCACTG  
 TGCCGGGCCGCTCCCTCTGGAGTACAGTCTACTCCCTCTCCCTGGTATTTCAGTGT  
 TGTGCTGAGAATTCTAGATACTACAGTTCTACTCCCTCTCCCTGGTATTTCAGTGT  
 ACCAGGATGGCGGGAGGGATCTGTGACTGTAGGTACTGTGCCAGGAAGGCTGGGTGAA  
 GTGACCATCTAAATTGCAAGGATGGTGAATTATCCCCATCTGTCTTAATGGGCTTACCTCCT  
 CTTTGCTTTGAECTCACTCAAAGATCTAGGCCTCATCTTACAGGTCTAAATCACTCAT  
 CTGGCCTGGATAATCTCACTGCCCTGGCACATTCCCTTGTGCTGTGGTGTATCCTGTGTT  
 TCCTTGCTGGTTG  
 TCTGTCTATTGTATCTGGACACAAGTCCTAAGTAGAGCAAGAATTCAACCAGCT  
 GCCTCTGTTCTACCTCACGACGTACCATCTGTCTTTGTGTGTGTGTGTGTG  
 TTGTTTTGCTTTACCAAACATGTCTGAAATCTAACCTCCTGCCAGGATTGTACA  
 GCATCTGGTGTGCTTATAAGCCAATAATTCAATGTGAAAAAAAAAAAAAA

## **FIGURE 134**

MRWILFIGALIGSSICGQEKFQGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFNR  
PVDVLVPSVSLQAFKSFLRSQGLEYAVTIEDLQALLDNEDEMHQHNEGQERSNNFNYGAYH  
SLEAIYHEMDNIAADFPDLARRVKIGHSFENRPMYVLKFSTGKVRRPAVWLNA  
GIHSREWI  
SQATAIW TARKIVSDYQRDPAIT SILEKMDIFLLPVANPDGYVYTQTQNRLWRKTRSRNPGS  
SCIGADPNRWNNASFAGKGASDNPCSEVYHGPHANSEVEVKSVD  
FIQKHGNFKGFIDLHSY  
SQLLMYPYGVSVKKAPDAEELDKVARLA  
AKALASVSGTEYQVGPTCTTVYPASGSSIDWAYD  
NGIKFAFTFELRDTGYGFLLPANQIIP  
TAETWLGLKTIMEHVRDNLY

**Signal peptide:**

amino acids 1-16

## **FIGURE 135**

## **FIGURE 136**

MASLYGVLFAGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLE  
TPSQNIFFPSPSVSTSLAMLSQLGAHSVTKTQILQGLGFNLHTPESAIHQGFQHLVHSLTVP  
SKDLTLKMGSALFVKKELQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQGK  
VVDIIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMMHQKEQFAF  
GVDTELNCFLQMDYKGDAVAFFVLPSPKGKMRQLEQALSARTLIKWSHSLQKRWIEVFIPRF  
SISASYNLETILPKMGIQNAFDKNADFGIAKRDSLQVSKATHKAVLDVSEEGTEATAATT  
KFIVRSKDGPSYFTVSFNRTFLMMITNKATDGILFLGKVENPTKS

**Signal peptide:**

amino acids 1-20

## **FIGURE 137**

## **FIGURE 138**

MKMQKGNVLLMFGLLLHLEAATNSNETSTSANTGSSVISSGASTATNGSSVTSSGVSTATI  
SGSSVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSE  
SSTPSSGASTVTNGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSS  
TTSSGASTATNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTT  
SNGAGTATNSESSTTSSGASTATNDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSS  
GASTATNDSSTTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGA  
NTATNSESSTVSSGASTATNSESSTTSSGVSTATNSESSTTSSGASTATNDSSTTSSEAST  
ATNSESSTVSSGISTVTNSESSTTSSGANTATNGSSVTSAGSGTAALTGMHTTSHSASTAV  
SEAKPGGSLVPWEIFLITLVSVVAAVGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGP  
GPGGNHGAPHRPRWSPNWFWRPVSSIAMEMSGRNSGP

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 510-532

**FIGURE 139**

GGGAGAGAGGATAAATAGCAGCGTGGCTCCCTGGCTCCTCTGCATCCTCCGACCTTC  
CCAGCAATATGCATCTTGACGTCTGGCGGCTCCTGCTCCCTCTGCTACTGGGGGCC  
CTGCTGGATGGCGGCCAGCGATGACCCCATTGAGAAGGTATTGAAGGGATCAACCGAGG  
GCTGAGCAATGCAGAGAGAGAGGTGGCAAGGCCCTGGATGGCATCAACAGTGGAAATCACGC  
ATGCCGGAAGGGAAAGTGGAGAAGGTTTCAACGGACTTAGAACATGGGAGCCACACCGGC  
AAGGAGTTGGACAAAGCGTCCAGGGCTCAACCACGGCATGGACAAGGTTGCCATGAGAT  
CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGTCAACAAACG  
CTGCTGGACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGTCCAC  
CAGGCTGGGAAGGAAGCAGAGAAACTTGGCCAAGGGTCAACCATGCTGCTGACCAGGCTGG  
AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCACCATGCTGCTGGCCAGGCCGGGAAGGAGC  
TGCAGAATGCTATAATGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGC  
AACCATCAAAGCGGATCTCCAGCCATCAAGGAGGGCCACAACCACGCCGTTAGCCTCTGG  
GGCCTCAGTCAACACGCCCTTCATCAACCTCCGCCGTGGAGGAGCGTCGCCAACATCA  
TGCCCTTAAACTGGCATCCGGCCTTGCTGGAGAATAATGTCGCCGTTGTCACATCAGCTGAC  
ATGACCTGGAGGGTTGGGGTGGGGACAGGTTCTGAAATCCCTGAAGGGGGTTGACTG  
GGATTGTGAATAAACTTGATAACACCA

## **FIGURE 140**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675
><subunit 1 of 1, 247 aa, 1 stop
><MW: 25335, pI: 7.00, NX(S/T): 0
MHLARLVGSCSLLLLL GALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAG
REVEKVFNGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAG
QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHAAAGQAGKELQN
AHNGVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**Homologous region to circumsporozoite (CS) repeats:**

amino acids 35-225

## **FIGURE 141**

CTCCGGGTCCCCAGGGGCTGGCAGGGGGCGGCTGGCAAGGGGGACGAGTCAGTGGACACTCCAGGAAGAGCGGG  
CCCAGGGGGCGATGACCGTGCCTGACCTGACTCACTCCAGGTCCGGAGGCAGGGGCCGGGGCGACTCG  
GGGGCGGACCAGCAGGGCGAGCTGCCGCCGTGAGTCGGCCAGGCCACCTGAGCCGAGCCGGACACCGTC  
GCTCTGCTCTCGAATGCTGCACCGCATGGGCTGAGGAGCTGGCTCGCCGCCCATGGGCGCCTGGCGCTGCC  
CCTCGGCCACCGCTGCTGCTCCTGCTGCTGCTCCTGCTGCAGCCGCCCTCGACCTGGCGCTCAGC  
CCCCGATCAGCCTGCCTCTGGCTCTGAAGAGCGGCCATTCTCAGATTGAAGCTGAACACATCTCAA  
ACAGCCCTCTGCTGAGCAGGGATGGCAGGACCTGTACGTGGGTGCTCGAGAGGCCCTTTGCACTCAGTAGC  
AACCTCAGCTTCTGCCAGGGGGAGTACCAAGGAGCTGTTGGGTGAGACGCAGAGAAGAAACAGCAGTG  
AGCTTCAAGGGCAAGGACCCACAGCGCAGTCAGGAACTACATCAAGATCCTCCTGCCGCTCAGCGGAGTC  
CTGTTCACCTGTGCACAGCAGCCTCAGCCCCATGTGTACCTACATCAACATGGAGAACTTCACCCCTGGCAAGG  
GAGCAGAAGGGAAATGTCTCTGGAAAGATGGCAAGGGCGTTGTCCTCGACCCGAATTCAAGTCCACTGCC  
CTGGTGGTTGATGGCAGCTACACTGGAACAGTCAGCAGCTCCAAGGGAAATGACCCGCCATCTCGGGAGC  
CAAAGCCTCGCCCCACCAAGACCGAGAGCTCCCTCAACTGGCTGCAAGACCCAGCTTGTGCCCTCAGCCTAC  
ATTCTGAGAGCCTGGGAGCTTGCAAGGGCATGATGACAAGATCTACTTTTCTTCAGCGAGACTGGCAGGAA  
TTTGAATTCTTGAGAACACCAATTGTGTCCCGCATGCCGCATCTGCAAGGGCATGAGGGTGGAGAGCGGGTG  
CTACAGCAGCGCTGGACCTCCCTCTCAAGGCCAGCTGCTGTGCTCACGGCCGACGATGGCTTCCCTCAAC  
GTGCTGAGGATGTTCACGCTGAGCCCCAGGCCAGGACTGGCGTACACCTTTCTATGGGTCTTCACT  
TCCCACTGGCAGGGAAACTACAGAAGGCTGCGCTGTTGCTTCAACATGAAGGATGTGAGAGACTTCTC  
AGCGGCCCTCATAAGGAGGTGAACCGTGGAGACACAGCAGTGGTACACCGTGACCCACCGGTGCCACACCCGG  
CCTGGAGCGTGCATCACCAACAGTGGCCGGGAAAGGAAGATCAACTCATCCCTGCACTTCCAGGCCGTGCTG  
AACTTCTCAAGGACCACTTCTGATGGACGGGCAAGTGGCAAGCGCATGCTGCTGTGCAAGCCCCAGGCTCG  
TACCAAGCGCTGGCTGTACACCGCTCCCTGGCTGCACCAACACTACGATGCTCTTCTGGGACTGGTAC  
GGCCGGCTCCACAAGGAGCTGAGCGTGGGCCCCCGGTGCACATCATTGAGGAGCTGCAGATCTCTCATCGGG  
CAGCCCGTGCAGAACTGCTCTGGACACCCACAGGGGCTGTTGATGCCCTCACACTCGGGCTAGTCCAG  
GTGCCCATGGCAACTGCAGGCTGTACCGGAGCTGTTGGACTGCCCTCCGGGAGCCACTGTGCTTGG  
AGCGGCTCCAGCTGCAAGCACGTAGCCTCTACAGGCTCAGTGGCCACCAGGGCGTGGATCCAGGACATCGAG  
GGAGCCAGCGCAAGGACCTTGCAGCGCTTCTGGTTGTGCCCCGTCTTGTACCAACAGGGGAGAAGCCA  
TGTGAGCAAGTCCAGTCCAGGCCAACACAGTGAACACTTGGCTGCCCTCTCAACACTGGCGACCCGA  
CTCTGGCTACGCAACGGGCCCCGTCAATGCCCTGGCTCCTGCCACGTGCTACCAACTGGGACCTGCTG  
GTGGGCAACAGCTGGGGAGTTCACTGCTGGTCACTAGAGGAGGGCTTCCAGCAGTGGTAGCCAGCTAC  
TGCCCAGAGGTGGTGGAGGACGGGTGGAGACACAAACAGATGGGGTGGCAGTGTACCGTCAATTACAGCACA  
TCGCGTGTGAGTCACAGCTGGCAAGGCCAGTGGGTGCAAGACAGGTCTACTGGAAAGAGTTCTGGT  
ATGTGACGCTTTGTGCTGCCGTGCTGCCAGTTTATTCTGCTTACCGGACCGAACAGCATGAAA  
GTCTTCTGAAGCAGGGGAATGTGCCAGCGTGCACCCCAAGACCTGCCCTGTTGCTGCCCTGAGACCCGC  
CCACTCAACGGCTTAAGGCCCCCTAGCACCCCGCTCGATCACCAGGGTACAGTCCCTGTCAGACAGCCCCCG  
GGGGCCGAGTCTCACTGAGTCAGAGAACAGGCCACTCAGCATCCAAGACAGCTCGTGGAGGTATCCCAGTG  
TGGGGCCCCGGGCCCCGGTCCGCTTGGCTGGAGATCCGTGACTCTGTGGTGTGAAGCTGACTTCCAGAGGACGC  
TGCCCCCTGGCTTCAAGGGCTGTGAATGCTGGAGAGGGTCAACTGGACCTCCCTCCGCTCTGCTTCTGG  
ACGACCGTGGTGGCCGGCCCTTGGGAGCCCTGGAGCCAGCTGCCCTGCTGCTCTCCAGTCAGTAGCGAAGCTCC  
TACCAACAGCACCAACAGCCGTGGGCCAGAGGTCTCTGCCAAATATGGGGCCTGCCAGTGGTGGAA  
CACTGCTCTTATGTAACAGGCCCTTGTAAAAAAACAAATTCCAATGTGAAACTAGAAATGAGAGGGAAAGAG  
ATAGCATGGCATGCCAGCACACAGCGTCTCCAGTCATGCCCTCCAGGGTCTGGGATGCATCCAAAGTGG  
TTGCTGAGACAGAGTTGAAACCCCTCACCAACTGCCCTTCCACATTATCCGCTGCCACCGGGCTGC  
CCTGCTCTACTGCAATTAGGACCCAGCTTGGGCTGCCGTGCTGCCCTGCCAGTCAGCCGAGGATGTAGTTG  
TTGCTGCCGTGCTCCACCACTCAGGGACCAAGGGCTAGGTGGACTGCCCTCACCAGGTCTGGGCTC  
GGACCCAACCTCTGGACCTTCCAGCGTGTATCAGGCTGTTGGGACACAGGAGAGGACAGCCGAGCTCAGGAGAGA  
TTTCTGACAATGTACGCCCTTCCCTCAGAAATTAGGAGAGAGACTGTCGCCCTGCCCTCCTCCGGTGTGCGTGA  
GAACCCGTGTGCCCTTCCACCATATCCACCCCTGCCCTCATTTGAAACTCAAACAGGAGAACTAAGTGAC  
CTGGCTCTCCCCAGTCCCCAGTTCACCCCTCCACCTCCACTCTAACGGGATATCAACACTGCC  
AGCACAGGGCCCTGAATTATGTTTATACATTAAAGATGCACTTATGCTATTAAATAAA

**FIGURE 142**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962
><subunit 1 of 1, 837 aa, 1 stop
><MW: 92750, pI: 7.04, NX(S/T): 6
MLRTAMGLRSWLAAPWGALPPRPLL LLLLQPPPPTWALSPRISLPLGSEERPFLRF
EAEHISNYTALLLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELLWGADAEEKQQCSFKG
KDPQRDCQNYIKILLPLSGSHLFTCGTAAFSPMCTYINMENFTLARDEGNVLLEDGKGRC
FDPNFKSTALVVDGELYTGTVSSFQGNDPAISRQSRLRPTKTESSLNLQDPAFVASAYIPE
SLGSIQGDDDKIYFFFSETGQEFEFFENTIVSRIARIICKGDEGGERVLQQRWTSFLKAQLLC
SRPDDGFPFNVLQDVFTLSPSPQDWRTLFYGVFTSQWHRGTTEGSACVFTMKDVQRVFSG
LYKEVNRETQQWYT VTHPVPTPRPGACITNSARERKINSSLQLPDRVLFNFKDHFLMDGQVR
SRMILLQHQARYQRVAVHRVPGLHHTYDVLFLGTGDGRHLHKAVSVGPRVHIIEELQIFSSGQ
PVQNLLLDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSLYQP
QLATRPWIQDIEGASAKDLCASSVVSPSFVPTGEKPCEQVQFQPNTVNTLACPLLSNLATR
LWLRNGAPVN ASASCHV LPTG D L L V GTQQLGEFQCWSLEEGFQQLVASYCPEVVEDGVADQ
TDEGGSVPVIISTSRVSAPAGGKASWGADRSYWK EFLVMCTL FVLAVLLPVLFLLYRH RNSM
KVFLKQGECASVHPKTCVVLPPETRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFT ESEKR
PLSIQDSFVEVSPVCPRPRVRLGSEIRDSVV
```

**Transmembrane domains:**

amino acids 23-46 (type II), 718-738

## **FIGURE 143A**

**FIGURE 143B**

TTAATTTATATTCTTACTGTTACTAAATATTAAGTGTCTTGACAATTTGGTGCTCATGTGTTGG  
GACAAAAGTGAATGAATCTGCATTATACCAGAAAGTTAAATTCTCAGATCAAATGTGCCTTAATAAATTGTT  
TTCATTTAGATTCAAACAGTGATAGACTTGCCATTTAACACGTCATTGGAGGGCTGCGTATTTGTAATAG  
CCTGATGCTATTGGAAAATAAACAGTGAACAATATTTCTATTGACTTTCGAACCAACACGAAAAAA  
ATTCCGTAGCTGAAGAATTGTATTACATTGGAGAGTAAAAACTAAACACGAAAAAA

**FIGURE 144**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836  
><subunit 1 of 1, 802 aa, 1 stop  
><MW: 91812, pI: 9.52, NX(S/T): 3  
MAARGRRRAWLSVLLGLVLGFVLASRLVLPRASELKAGPRRRASPEGCRSGQAAASQAGGAR  
GDARGAQLWPPGSDPDGGPRDRNFLFVGVMTAQKYLQTRAVAAYRTWSKTIPGVQFFSSEG  
SDTSVPPIPVVPLRGVDDSYPPQKKSFMMLKYMHDHYLDKYEWFMRADDDVYIKGDRLENFLR  
SLNSSEPLFLGQTGLGTTEEMGKLAEPGENFCMGGPGVIMSREVLRRMVPHIGKCLREMYT  
THEDVEVGRCVRRFAGVQCVWSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLHPNKNPP  
YQYRLHSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEQLQLGIPPSFMRFQPRQREE  
ILEWEFLTGKYLYSAVDGQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQY  
GYRRVNPAMYGAEYILDLLLLYKKHKKGKKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKR  
INQESGSLSFLNSNLKKLVPFQLPGSKSEHKEPKDKKINILIPLSGRFDMFVRFMGNFEKTC  
LIPNQNVKLVLLLNFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQ  
FNNESSLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSDNHFAFT  
QKTGFWRNYGFGITCIYKGDLVRVGGFDVSIQGWGLEDVDLFNKVVQAGLKTFRSQEVGVVH  
VHHPVFCDPNLDPKQYKMCLGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA

**Signal peptide:**

amino acids 1-23

## **FIGURE 145**

GGACAACC GTT GCT GGG GTCC CAGGC CTG AGGC AGG AC GG TACT CC GCT GAC AC CCT CCC  
 TT CCG GC TTG AGG GTCC CAGC CTG GTGG CCCC CAGG AC GTT CGC ATGG CAG AGT GCT  
 ACGG AC GAC GC CT **ATGA** AGC CCT TAG CTT CTAG TT GCG CTT GCT ATGG CTT CGT CTG  
 TGCC GG CT TATCC GAG CATA ACT GTG ACAC CTG ATGA AGAG CAAA ACT TGA ATC ATT ATATA  
 CAAG TTT AGAGA ACCT AGTAC GAAGT GTT CCCT GTGG GAG CCAG GT CGT GAG AAAA AATC  
 TAACT CT CCAAA ACAT GTT ATT CTAT AGCAT CAAAG GG AT CAAA ATT TAAGG AGC TAG TTA  
 CACAT GGAGAC GCTT CAACT GAGA ATGAT GTT TAACCA AT CCT AT CAGT GAAG AA ACT ACA  
 ACT TT CCCT ACAGG AGG CTTCAC ACCGG AAATAGG AAAG AAAA ACAC CGG AAAGT ACCCC  
 ATT CTGG TC GAT CAA ACCA AAACA AT GTT CCATT GTT GAT GCAG AGG AAC CT TAT ATT G  
 AAAA ATGA AGAG GCC CAG AGC CAG AGC CCG AGC CAG CTG CAA AAC AA ACT GAGG CACCA AGA ATG  
 TTGCCAGTTGTTACTGAATCATCTACAGTCCATATGTTACCTCATACAGTCACCTGTCAC  
 CACTT TAGATAAGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCCCTCAGCTCT  
 CAGGTGAAACTGCGATAGAAAAACCGAAGAGTTGGAAAGCACCCAGAGAGTTGGAATAAT  
 GATGACATTTGAAAAAAATTAGATATTAATTACAAGTGCAACAGGC ACTT CTTAGTGA  
 CACCAGCAACCCAGCATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAACGAAGCC  
 TTGCTCTAGCAGCAGCAGCAGAACATAAATTAAAAACAAATGTATAAGTCCCAGTTATTGCCA  
 GTAGGACGAACAAGTAATAAAATTGATGACATCGAAACTGTTATTACATGCTGTGTAATT  
 TAGATCTAAACTCTATGAATATTAGATATTAAATGTGTTCCACCAGAGATGAGAGAAAAAG  
 CTGCTACAGTATTCAATACATTAAAAAATATGTGTAGATCAAGGAGAGTCACAGCCTTATTA  
 AAAGTTAT**TAA**ACAATAATATAAAATTAAACCTACTTGATATTCCATAACAAAGCTGA  
 TTTAAGCAAAC TG CATT TTT CACAGG AGA ATA ATC AT TCG TA ATT CAA AAC AGT GTAT  
 AAAA AT ATT TT CT ATT GTAG TT CAA AT GTGCC AAC AT CTT AT GTG T CAT GTG TT ATG AACA  
 ATT TT CAT AT GCA CT AAA ACCT AATT AAA ATT TT GG TT CAGG AAAA

**FIGURE 146**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864
><subunit 1 of 1, 350 aa, 1 stop
><MW: 39003, pI: 5.59, NX(S/T): 1
MKPLVLLVALLLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRSPSGEPGREKKNSPK
HVYSIASKGSKFKELVTHGDASTENDVLTNPISEETTFPTGGFTPEIGKKKTESTPFWSI
KPNNVSIVLHAEPYIENEPEPEPAAKQTEAPRMLPVVTESSSTSPYVTSYKSPVTLDK
STGIEISTESEDVPQLSGETAIEKPEEFGKHPESWNNDILKKILDINSQVQQALLSDTSNP
AYREDIEASKDHLKRSILALAAAEEHKLKTMYKSQLLPVGRTSNKIDDIETVINMLCNSRSKL
YEYLDIKCVPPEMREKAATVFNTLKNMCRSRRVTALLKVY
```

**Signal peptide:**

amino acids 1-19

## **FIGURE 147**

CGGCTCGAGCGGCTCGAGTGAAGAGGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTG  
 ACCTCCAAATCATCCATCCACCCCTGCTGTCATCTGTTCATAGTGTGAGATCAACCCACA  
 GGAATATCC**ATG**CTTTGTGCTCATTGGTCTCAGTTCTACGAGCTGGTGTCAAGGACA  
 GTGGCAAGTCACTGGACCGGGCAAGTTGTCCAGGCCTGGTGGGGAGGACGCCGTGTTCT  
 CCTGCTCCCTTTCTGAGACCAGTGCAAGAGGCTATGGAAGTGCAGGTTCTCAGGAATCAG  
 TTCCATGCTGTTGACCTACAGAGATGGGGAAAGACTGGAAATCTAACAGAGATGCCACA  
 GTATCGAGGGAGAAGTGGAGACTGAGTTGTGAAGGACTCCATTGCAGGGGGCGTGTCTCTAAGGC  
 TAAAAAAACATCACTCCCTCGGACATCGGCTGTATGGGTGCTGGTTAGTCCCAGATTAC  
 GATGAGGAGGCCACCTGGGAGCTGCGGGTGGCAGCACACTGGGCTCACTCCTCTATTCCAT  
 CGTGGGATATGTTGACGGAGGTATCCAGTTACTCTGCCTGTCCTCAGGCTGGTCCCCCAGC  
 CCACAGCCAAGTGGAAAGGTCCACAAGGACAGGGATTGTCTTCAGACTCCAGAGCAAATGCA  
 GATGGGTACAGCCTGTATGATGGAGATCTCCATTATAGTCCAGGAAAATGCTGGGAGCAT  
 ATTGTGTTCCATCCACCTTGTGAGCAGAGTCATGAGGTGAATCAAAGGTATTGATAGGAG  
 AGACGTTTCCAGCCCTCACCTGGCGCTGGCTTCTATTACTCGGGTTACTCTGTGGT  
 GCCCTGTGTGGTGTGTCATGGGATGATAATTGTTCTCAAATCCAAAGGGAAAATCCA  
 GGCGGAACGGACTGGAGAAGAACGACGGACAGGCAGAATTGAGAGACGCCGGAAACACG  
 CAGTGGAGGTGACTCTGGATCCAGAGACGGCTACCCGAAGCTCTGCCTTCTGATCTGAAA  
 ACTGTAACCCATAGAAAAGCTCCCAGGAGGTGCTCACTCTGAGAAGAGATTACAAGGAA  
 GAGTGTGGTGGCTTCTCAGGGTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGAC  
 AAAATGTAGGGTGGTATGTGGAGTGTGCGGATGACGTAGACAGGGGAAGAACAAATGTG  
 ACTTTGTCTCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTGTATTTCAC  
 ATTCAATCCCCATTTCAGCCTCCCCCCCAGCACCCCTCTACACGAGTAGGGTCTTCC  
 TGGACTATGAGGGTGGACCATCTCTTCAATACAAATGACCAGTCCCTTATTATACC  
 CTGCTGACATGTCAGTTGAAGGCTTGTGAGACCCCTATATCCAGCATGCGATGTATGACGA  
 GGAAAAGGGGACTCCCATATTCATATGTCAGTGTCTGGGG**TGA**GACAGAGAACCCCTG  
 CTTAAAGGGCCCCACACCACAGACCCAGACACAGCCAAGGGAGGTGCTCCGACAGGTGGC  
 CCCAGCTCCTCTCGGAGCCTGCGCACAGAGACTCACGCCCTACTCTCCTTAGGGAGC  
 TGAGGTTCTCTGCCCCCTGAGCCCTGAGCAGCAGGGCAGTCACAGCTCCAGATGAGGGGGAT  
 TGGCCTGACCCCTGTGGGAGTCAGAACCCATGGCTGCCCTGAAGTGGGACGGAATAGACTCA  
 CATTAGTTTAGTTGTGAAAACATCCAGCTAACGATCTGAACAAGTCACAACCTCC  
 CAGGCTCCTCATTCAGTCACGGACAGTGATTCTGCCTCACAGGTGAAGAGATTAAAGAGA  
 CAACGAATGTGAATCATGCTTGAGGTTGAGGGCACAGTGTGCTATTGCTAATGATGTGTTTA  
 TATTATACATTTCACCATAAAACTCTGTTGCTTATTCCACATTAATTACTTTCTCTA  
 TACCAAATCACCCATGGAATAGTTATTGAACACCTGCTTGTGAGGCTAAAGAATAAAGAG  
 GAGGTAGGATTTCACTGATTCTATAAGCCCAGCATTACCTGATACCAAAACCAGGCAAAG  
 AAAACAGAAGAAGAGGAAGGAAAACATCACGGTCCATATCCCTCATTAACACAGACACAAAAAA  
 TTCTAAATAAAATTAAACAAATTAAACTAAACATATTAAAGATGATATATAACTACT  
 CAGTGTGGTTGTCCCACAAATGCAGAGTTGTTAATATTAAATATCAACCAGTGTAAATT  
 CAGCACATTAATAAAGTAAAAAGAAAACCATAAAAAAAAAAAAAAA

**FIGURE 148**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866
><subunit 1 of 1, 466 aa, 1 stop
><MW: 52279, pI: 6.16, NX(S/T): 2
MAFVLILVLSFYELVSGQWQVTGPGKFWQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHA
VVHLYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEE
ATWELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGY
SLYDVEISIIIVQENAGSILCSIHLAEQSHEVESKVLIGETFFQPSPWRLASILLGLLCALC
GVVMGMIIIVFFSKKGKIQAELDWRRKHGQAEELRDARKHAVEVTLDPETAHPKLCVSIDLKTVT
HRKAPQEVPHSEKRFRKSVASQGFQAGRHYWEVDVGQNVGWWYVGVCRDDVDRGKNNVTLS
PNNGYWVLRLTTEHLYFTFNPHFISLPPSTPPTRGVFLDYEGGTISFFNTNDQSLIYTLT
CQFEGLLRPYIQHAMYDEEKGTPIFICPVSWG
```

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 131-150, 235-259

## **FIGURE 149**

CCTTCACAGGACTCTCATTGCTGGTGGCA**ATG**ATGTATCGGCCAGATGTGGTGA  
 GGAAAAGAGTTGTTGGAACCTGGTTATCGGCCTCGTCATCTCATATCCCTGATTGTC  
 CTGGCAGTGTGCATTGGACTCACTGTTCATTATGTGAGATATAATCAAAGAACCTACAA  
 TTACTATAGCACATTGTCATTACAACGTACAAACTATATGCTGAGTTGGCAGAGAGGCTT  
 CTAACAATTTACAGAAATGAGCCAGAGACTTGAATCAATGGTAAAAATGCATTATAAA  
 TCTCCATTAAGGAAAGAATTGTCAGTCTCAGGTATCAAGTTCAACAGAACGCATGG  
 AGTGGTGGCTCATATGCTGTTGATTGAGATTTCACTCTACTGAGGATCCTGAAACTGTAG  
 ATAAAAATTGTTCAACTGTTTACATGAAAAGCTGCAAGATGCTGAGGACCCCTAAAGTA  
 GATCCTCACTCAGTTAAAATTAAAAAAATCAACAAAGACAGAAACAGACAGCTATCTAAACCA  
 TTGCTGCGAACACGAAGAAGTAAAACCTCTAGGTAGGTCTCAGGATCGTTGGTGGACAG  
 AAGTAGAAGAGGGTGAATGCCCTGGCAGGCTAGCCTGCAGTGGATGGAGTCATCGCTGT  
 GGAGCAACCTTAATTATGCCACATGGCTTGAGTGCTGCTCACTGTTACAACATATAA  
 GAACCTGCCAGATGGACTGCTCCTTGGAGTAACAATAAACCTCGAAAATGAAACGGG  
 GTCTCCGGAGAATAATTGTCATGAAAATACAAACACCCATCACATGACTATGATATTCT  
 CTTGCAGAGCTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTGTCTCCCTGA  
 TGCACTCCTATGAGTTCAACCAGGTGATGTGATGTTGTGACAGGATTGGAGCACTGAAAA  
 ATGATGGTTACAGTCAAAATCATCTCGACAAGCACAGGTGACTCTCATAGACGCTACAACT  
 TGCAATGAACCTCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTT  
 AGAAGGAAAAACAGATGCATGCCAGGGTGAECTGGAGGACCACTGGTAGTTCAAGATGCTA  
 GAGATATCTGGTACCTTGCTGGAATAGTGAGCTGGGAGATGAATGTGCAAAACCCAACAAG  
 CCTGGTGTACTAGAGTTACGGCCTGCGGACTGGATTACTTCAAAACTGGTATC**TA**  
**A**GAGACAAAAGCCTCATGGAACAGATAACATTTTTTGTTTTGGGTGTGGAGGCCATT  
 TTTAGAGATAACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTTGACTGATCTCAATAAAC  
 TGTTGCTGATGCATGTATTTCTTCCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTG  
 CCAGATCAACTCTGTCATCTGTGAGCAATAGTTGAAACTTATGTACATAGAGAAATAGATA  
 ATACAATATTACATTACAGCCTGTATTCAATTGTTCTCTAGAAGTTGTCAAGATTGAC  
 TTGTTGACATAAATTGTAATGCATATATAACAATTGAAGCACTCCTTCTTCAGTTCTC  
 AGCTCCTCTCATTCAGCAAATATCCATTTCAGGTGCAGAACAGGAGTGAAAGAAAATA  
 TAAGAAGAAAAAAATCCCTACATTATTGGCACAGAAAAGTATTAGGTGTTCTTAGT  
 GGAATATTAGAAATGATCATATTCAATTGAAAGGTCAAGCAAAGACAGCAGAACATCAAC  
 ACTTCATCATTAGGAAGTATGGAACTAAGTTAAGGAAGTCCAGAAAGAACGCAAGATATA  
 TCCTTATTTCATTCACAAACTACTATGATAATGTGAAGAAGATTCTGTTTTGTG  
 ACCTATAATAATTACAAACTCATGCAATGTACTTGTCAAGCAAATTAAAGCAAATAT  
 TTATTAAACATTGTTACTGAGGATGTCAACATATAACAATAAAATATAACACCCCA

**FIGURE 150**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871
><subunit 1 of 1, 423 aa, 1 stop
><MW: 47696, pI: 8.96, NX(S/T): 3
MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYYSTLSFTTD
KLYAEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSSQQKHGVLAHMLLICR
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTL
GQSLRIVGGTEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFG
VTIKPSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSPVPTNAVHRVCLPDASYEFQPGDV
MFVTGFGALKNDGYSQNHLRQAQVTLIDATTNEPQAYNDAITPRMLCAGSLEGKTDACQGD
SGGPLVSSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI
```

**Transmembrane domain:**

amino acids 21-40 (type II)

**FIGURE 151**

GTCGAAGGTTATAAAAGCTTCCAGCAAACGGCATTGAAGTTGAAGATACAACCTGACAGCA  
CAGCCTGAGATCTTGGGGATCCCTCAGCCTAACACCCCACAGACGTAGCTGGTGGATTCCCG  
CTGCATCAAGGCCTACCCACTGTCTCC**ATG**CTGGCTCTCCCTGCCTCTGTGGCTCTGGC  
CGTGACCTTCTTGGTTCCCAGAGCTCAGCCCTTGGCCCTCAAGACTTGAAGAAGAGGGAGG  
CAGATGAGACTGAGACGGCGTGGCCGCCCTTGCCGGCTGTCCCCTGCGACTACGACCAGTC  
CGACACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGGTCGGGCCGGCCTGCCTGTGCC  
AGGACTCTCCAGCCCCGCCAGCCGCCGACCCGCCGCATGGGAGAAGTGCAGCATTGCC  
CCGAAGAGGGCCGCGCAGTGGTCCACTGGTGTGCCCTTCTCCCCGGTCCTCCACTACTGG  
CTGCTGCTTGGGACGGCAGCGAGGCTGCGCAGAAGGGGCCCGCTGAACGCTACGGTCCG  
CAGAGCCGAACTGAAGGGCTGAAGCCAGGGGCATTATGTCGTTGCGTAGTGGCCGCTA  
ACGAGGCCGGGCAAGCCGCGTCCCCAGGCTGGAGGAGAGGGCCTCGAGGGGCCGACATC  
CCTGCCTTCGGGCCTTGCAGCCGCTTGCAGGCCAACCCCCGCACTCTGGTCCACGC  
GGCCGTGGGTGGGCACGGCCCTGGCCCTGCTAAGCTGTGCCGCCCTGGTGTGGCACTTCT  
GCCTGCGCGATCGCTGGGCTGCCCGCCGAGCCGCCGAGCCGAGGGCGCTC**TGA**  
AAGGGCCTGGGGCATCTCGGGCACAGACAGCCCCACCTGGGGCGCTCAGCCTGGCCCCG  
GGAAAGAGGAAAACCCGCTGCCTCCAGGGAGGGCTGGACGGCGAGCTGGAGGCCAGCCCCAG  
GCTCCAGGGCACGGCGAGTCATGGTCTCAGGACTGAGCGCTTGTAGGTCCGGTACTT  
GGCGCTTGTTCCTGGCTGAGGTCTGGGAAGGAATAGAAAGGGCCCCAATTTTTTA  
AGCGGCCAGATAATAATGTAACCTTGCAGTTAAAAAAA

## **FIGURE 152**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874
><subunit 1 of 1, 238 aa, 1 stop
><MW: 25262, pI: 6.44, NX(S/T): 1
MLGSPCLLWLLAVTFLVPRAQPLAPQDFEEEADETETAWPPLPAVPCDYDHCRHLQVPCKE
LQRVGPAACLCGPLSSPAQPPDPRMGEVRIAAEEGRAVVHWCAPFSPVLHYWLLLWDGSEA
AQKGPPLNATVRRAELKGLKPGGIYVVCVVAANEAGASRVPQAGGEGLEGADIPAFGPCSRL
AVPPNPRTLVHAAGVGTALALLSCAALVWHFCLRDRWGCPRRAAARAAGAL
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 194-220

**N-glycosylation site.**

amino acids 132-135

## **FIGURE 153**

AGAGAAAGAACGCTCCAGCTGAAGCCAATGCAGCCCTCGGCTCTCCGCGAAGAAGTTCC  
 CTGCCCGATGAGCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGGTGGGCACCGGG  
 CCCAGCGCCGACGATCGCTGCCGTTGCCCTGGGAGTAGGATGTGGTGAAAGGATGGGG  
 TTCTCCCTACGGGCTCACAA**ATG**GCCAGAGAAGATTCCGTGAAGTGTCTGCCTGC  
 CTACGCCCTCAATCTGCTCTTGGTAATGTCCATCAGTGTGTTGCAGTTCTGCTGG  
 TGAGGGACTACCTAATAATGTTCTCACCTTAAC TGAGAAACGAGGGTAGAGGAAGCAGTC  
 ATTTGACTTACTTCTGTGGTCATCCGGCATGATTGCTGTTGCTGTTCCATTATCAT  
 TGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAACTGTTGCTTGCATGGTACT  
 TTGGAAGTTGCTTGTCACTTCTGTGTTAGAAGTGGCTGTGGCGTTGGACATATGAACAG  
 GAACTTATGGTCCAGTACAATGGTCAGATATGGTCACTTGAAAGGCCAGGATGACAAATTA  
 TGGATTACCTAGATATCGGTGGCTACTCATGCTGGAATTTCAGAGAGAGTTAAGT  
 GCTGTGGAGTAGTATATTCACTGACTGGTTGAAATGACAGAGATGGACTGGCCCCAGAT  
 TCCTGCTGTGTTAGAGAATTCCCAGGATGTTCAAACAGGCCACCAGGAAGATCTCAGTGA  
 CCTTATCAAGAGGGTTGTTGGAAAGAAAATGTATTCCATTGGGTGACACAAATCCTGGCCATGATTCTCACC  
 AGGTGCTGAGGTTCTGGGAATCTCCATTGGGTGACACAAATCCTGGCCATGATTCTCACC  
 ATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGGACAGACCAAATGATGTC  
 CTTGAAAGAATGACAACCTCAGCACCTGTCATGTCCTCAGTAGAAGTGTGAAACCAAGCC  
 TGTCAAGAATCTTGAACACACATCCATGGCAAACAGCTTAATACACACTTGGAGATGGAG  
 GAGTTA**TAAA**AAGAAATGTCACAGAAGAAAACCACAAACTTGTATTGGACTGTGAATT  
 TTTGAGTACATACTATGTTGTTAGAAATATGAGAAATAAAATGTTGCCATAAAATAACA  
 CCTAAGCATATACTATTCTATGCTTAAATGAGGATGGAAAAGTTCATGTCATAAGTCAC  
 CACCTGGACAATAATTGATGCCCTTAAATGCTGAAGACAGATGTCATACCCACTGTGTAGC  
 CTGTGTATGACTTTACTGAACACAGTTATGTTGAGGCAGCATGGTTGATTAGCATT  
 CGCATCCATGCAAACGAGTCACATATGGGGACTGGAGCCATAGTAAAGGTTGATTACT  
 CTACCAACTAGTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATA  
 ACTTTATTACTCAGCGATCTATTCTGATGCTAAATAATTATATCAGAAAACCTTC  
 AATATTGGTGAACACATTGTGATTTGCTGGTTACTAAAATATTCTTACCACTAAAAA  
 GAGCAAGCTAACACATTGTCTTAAGCTGATCAGGGATTGGTATATAAGTCTGTGTTAA  
 TCTGTATAATTCACTGATTTCTGATAATGTTAGAATAACCATTATGAAAAGGAAA  
 ATTGTCCTGTATAGCATCATTATTTAGCCTTCCTGTTAAAGCTTACTATTCTGT  
 CCTGGGCTTATATTACACATATAACTGTTATTAATACTTAACCACTAATTGAAAATTA  
 CCAGTGTGATACATAGGAATCATTATTCAAGATGTAGTCTGGTCTTAGGAAGTATTAATAA  
 GAAAATTGACATAACTTAGTGATTCAAGAAAGGACTTGTATGCTGTTCTCCAAATG  
 AAGACTCTTTGACACTAACACTTTAAAAAGCTTATCTTGCCCTCTCCAAACAAAGAA  
 GCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTCTTTCTCCAGAAAAAT  
 GCTTGTGAGAATCATTAAACATGTGACAATTAGAGATTCTTGTGTTATTCACTGATTA  
 ATATACTGTGGCAAATTACACAGATTATAAATTGTTACAAGAGTATAGTATATT  
 GAAATGGAAAAGTGCATTTACTGTATTGTTGTTATTCTCAGAATATGGAA  
 AGAAAATTAAATGTGTCATAAAATATTCTAGAGAGTAA

## **FIGURE 154**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880
><subunit 1 of 1, 305 aa, 1 stop
><MW: 35383, pI: 5.99, NX(S/T): 0
MAREDSVKCLRCLLYALNLLFWLMSISVLAWSAWMRDYLNNVLTLTAETRVEEAVILTYFPV
VHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQ
WSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVFWDWLEMTEMDWPPDSCCVREF
PGCSKQAHQEDLSLDLYQEGCGKMYSLRGTKQLQVLRFLGISIGVTQILAMILTITLLWAL
YYDRREPQTDQMMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL
```

**Signal peptide:**

amino acids 1-33

**Transmembrane domains:**

amino acids 12-35, 57-86, 94-114, 226-248

## **FIGURE 155**

GAGAGAGGCAGCAGCTGCTCAGCGGACAAGGATGCTGGCGTGAGGGACCAAGGCCTGCC  
 TGCACTCGGGCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGCCAGCCAGGA  
 CCTGTGTGGGGAGGCCCTCCTGCTGCCCTGGGTGACAATCTCAGCTCCAGGCTACAGGGAG  
 ACCGGGAGGATCACAGAGCCAGC**ATGTT**ACAGGATCCTGACAGTGTCAACCTCTGAACAGC  
 CTCGATGTCAAACCCCTGCGCAAACCCGTATCCCCATGGAGACCTCAGAAAGGTGGGAT  
 CCCCACATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTTGCCATCAAGG  
 TGATTCTGGATAAATACTACTTCCCTGCGGGCAGCCTCTCCACTTCATCCGAGGAAGCAG  
 CTGTGTGACGGAGAGCTGGACTGTCCCTGGGGAGGACGAGGAGCACTGTGTCAAGAGCTT  
 CCCGAAGGGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGG  
 ACTCGGCCACAGGGAACTGGTTCTCTGCCTGTTGACAACTTCACAGAACGCTCGCTGAG  
 ACAGCCTGTAGGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCAGACCAGGATCTGGA  
 TGTTGTTGAAATCACAGAAAACAGCCAGGAGCTCGCATCGGAACCTCAAGTGGGCCCTGTC  
 TCTCAGGCTCCCTGGTCTCCCTGCACTGTCTGCCGTGGGAAGAGCCTGAAGACCCCCCGT  
 GTGGTGGGTGGGAGGAGGCCTCTGTGGATTCTTGGCCTGGCAGGTACGCATCCAGTACGA  
 CAAACAGCACGTCTGGAGGGAGCATCCTGGACCCCCACTGGTCCTCACGGCAGCCCAGT  
 GCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCAGGCTCAGACAAACTGGC  
 AGCTTCCCATCCCTGGTGTGGCAAGATCATCATCATTGAATTCAACCCATGTACCCCAA  
 AGACAATGACATGCCCTCATGAAGCTGCAGTCCCACACTTCAGGCACAGTCAGGC  
 CCATCTGTCTGCCCTTCTTGATGAGGAGCTCACTCCAGCCACCCACTCTGGATCATGG  
 TGGGGCTTACGAAGCAGAATGGAGGGAAAGATGTCTGACATACTGCTGCAGGCGTCAGTCCA  
 GGTCAATTGACAGCACCGGTGCAATGCAGACGATGCGTACCGAGGGAAAGTCACCGAGAAAGA  
 TGATGTGTGCAGGCATCCCGAAGGGGTGTGGACACCTGCCAGGGTGACAGTGGTGGGCC  
 CTGATGTACCAATCTGACCAAGTGGCATGTGGTGGCATCGTAGCTGGCTATGGCTGCC  
 GGGCCCGAGCACCCAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATG  
 TCTGGAAGGCTGAGCT**TAA**TGCTGCTGCCCTTGCAGTGCTGGAGGCCCTCCTG  
 CCCTGCCACCTGGGATCCCCAAAGTCAGACACAGAGCAAGAGTCCCCTGGTACACCC  
 CTCTGCCACAGCCTCAGCATTCTGGAGCAGCAAAGGGCTCAATTCTGTAAGAGACCC  
 TCGCAGCCCAGAGGCAGGGAGACACAGCCCAGAGGAAGTCAGCAGCCCTAGCTGCCACACTGGTGCTCCC  
 AGCATCCCAGGGAGAGACACAGCCCAGAGGAAGTCAGCAGGCCCTAGCTGCCACACTGGTGCTCCC  
 GGAACCTTCCCACACTACTGAATGGAAGCAGGCTGTCTGTAAAAGCCCAGATCACTGTGG  
 CTGGAGAGGAGAAGGAAAGGGTCTGCCAGCCCTGTCCGTCTCACCCATCCCCAAGCCTA  
 CTAGAGCAAGAAACCAGTTGTAATATAAAATGCACTGCCACTGTGGTATGACTACCGTT  
 ACCTACTGTTGTCATTGTTATTACAGCTATGCCACTATTATAAGAGCTGTGTAACATCT  
 CTGGCAAAAAAAA

**FIGURE 156**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47644, pI: 5.18, NX(S/T): 2
MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVVLIKVILDKYYF
LCGQPLHFI PRKQLCDGELDCPLGEDEEHCVKSFP EGP AVAVRLSKDRSTLQV L DSATGNWF
SACFDNFTEAL AETACRQM GYSRAVEIGPDQDL DVVEITENSQEL RMRNSSGPCLSGSLVSL
HCLACGKSLKTP RVVGEEASV DSWPWQV SIQYDKQHVC GGSILD PHW VLTA AHCF RKHTDV
FNWKVRAGSDKLGSF PSLAVAK IIIIEFNPMYPKDNDIALMKLQFPLTFS GTVRP ICLP FFD
EELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPE
GGVDT CQGD SGGPLM YQSDQWHVV GIVSWGYGC GGPSTPGV YT KVSAYLNWIYNVWKAEL
```

**Transmembrane domain:**

amino acids 32-53 (typeII)

## **FIGURE 157**

GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGCATCCCAGGCTCCAG  
 AGCTCCCTGGTACAGTCTGGCTGAGC**ATGGCCCTCCAGCCCTGGCCTGGACCCCTGGAGCCTCTGGGCC**  
 TTTTCCCTTCCAAC TGCTCAGCTGCTGCCAGCAGACGCCGGGGAGGCAGGGCAGGGCCATGCCA  
 GGGTCAGATACTATGCAGGGATGAACGTAGGGACTTAGCTTCTCACCAGAAGGGCCTCAGGATTGACA  
 CTCTGCTCTGAGTGGTATGGAAATACTCTACGTGGGGCTCGAGAACGCCATTCTGGCCTGGATATCCAGG  
 ATCCAGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTA  
 AGAAGAAGAGCAATGAGACACAGTGTTCAACTTCATCCGTGCTGGTTCTTACAATGTCACCCATCTAC  
 CCTGGGCACCTTCGCCTCAGCCCTGCTTACCTCATTAAGATTCTACCTGTTGCCATCTCGG  
 AGGACAAGGTCAAGGAGGGAAAAGGCCAAAGCCCCTTGACCCGCTCACAGCATA CGCCTGCTGGGATG  
 GGATGCTCTATTCTGGTACTATGAACAACTTCCCTGGCAGTGAGCCCATTGATGCGCACACTGGGATCCCAGC  
 CTGTCCTCAAGACCGACAACCTCCCTGGCAGTGATCATGACGCCCTTGTGGCAGCCATCCCTCGACCC  
 AGGTCGCTACTTCTTCTCGAGGAGACAGCCAGCGAGTTGACTTGTGAGAGGCTCCACACATCGGGTGG  
 CTAGAGTCTGCAAGAATGACGTGGCGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTCCTGAAGGCCAGC  
 TGCTCTGCACCCAGCCGGGAGCTGCCCTCAACGTCATCCGCCACGCCCTGCTCCCCGCCGATTCTCCA  
 CAGCTCCCCACATCTACGCAGTCTCACCTCCAGTGGCAGGTTGGCGGGACCAGGAGCTGCGGTTGCGCT  
 TCTCTCTGGACATTGAACGTGTCTTAAGGGAAATAACAAAGAGTGAACAAAGAAACTTCACGCTGGACTA  
 CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGCCCTCCTGATAAGGCCCTGACCT  
 TCATGAAGGACCATTCTGATGGATGAGCAAGTGGTGGGAGCGCCCTGCTGGTGAATCTGGCGTGGAGTATA  
 CACGGCTTGCAGTGGAGACAGCCAGGGCTTGTGGCACAGCCATCTGTCATGTACCTGGGAACCACACAG  
 GGTGCGTCCACAAGGCTGTGTAAGTGGGACAGCAGTGCTCATCTGGTGGAGAGATTGAGCTGTTCCCTGACC  
 CTGAACCTGTTGCAACCTGCAGCTGGCCCCACCCAGGTGCAGTGTTGAGGCTCTCAGGAGGTGCTGG  
 GGGTGCCCGAGCCAACGTAGTGTCTATGAGAGCTGTGACTGTGCCCTGCCGGGACCCCCACTGTGCCT  
 GGGACCCCTGAGTCCGAACCTGTTGCCCTGTCTGCCCTAACCTGAAACTCTGGAAAGCAGGACATGGAGCGGG  
 GGAACCCAGAGTGGCATGTGCCAGTGGCCCATGAGCAGGAGCCTTGGCCTCAGAGCCGCCGAAATCATTA  
 AAGAAGTCCTGGCTGTCCCCACTCCATCCTGGAGCTCCCTGCCCTACCTGTCAGCCTGGCTCTTATTATT  
 GGAGTCATGGCCAGCAGCAGTCCAGAGCAGCTCTTCAACTGTCTACAATGGCTCCCTTGCTGATAGTCAGG  
 ATGGAGTTGGGGTCTTACCAAGTGTGGCAACTGAGAATGGCTTTCATACCTGTGATCTCTACTGGTGG  
 ACAGCCAGGACCAGCCCTGCCCTGGATCCTGAACTGGCAGGCATCCCCGGAGCATGTGAAGGTCCCGTTGA  
 CCAGGGCAGTGGGGCCGCCCTGGCTGCCAGCAGTCTACTGCCCTACTTGTCACTGTCACTGTCT  
 TTGCTTAGTGCTTCAAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCAGTCCGGCTGGGCAAGG  
 TTCAGGGCTGTGAGACCCCTGCCCTGGGAGAAGGCCCTGTTAAGCAGAGAGCAACACCTCCAGTCTCCAAGG  
 AATGCAGGACCTGCCAGTGATGTGGACGCTGACAACAACTGCCCTAGGCACTGAGGTAGCT**TAA**ACTCTAGGCA  
 CAGGCCGGGCTGCCGTGAGGACCTGGCCATGCTGGCTGGCAGGCCAAGCAGGCCCTGACTAGGATGACAG  
 CAGCACAAAAGACCACCTTCTCCCTGAGAGGAGCTTGCTACTGTCATGACACTCAGCAGGGTG  
 ATGCACAGCAGTGCCTCCCTATGGACTCCCTACCAAGCAGCATGAGCTCTAACAGGGTGGGGCTAC  
 CCCCAGACCTGCTCTAACACTGATATTGAAGAACCTGGAGAGGATCCTCAGTTCTGGCATTCCAGGGACCC  
 CAGAAACACAGTGTTCAGAGACCCCTAAAAAACCTGCCCTGCTCCCAGGACCCATTGTAATGAACACCAAACATC  
 TAAACAATCATATGCTAACATGCCACTCCCTGGAAACTCCACTCTGAAAGCTGCCCTGGACACCAACACTCC  
 TCTCCCAAGGTCTGAGGATCTGCTCCCTCCTGCTTACCAAGTGTGACCCGCTGACTCCAGGAAGTC  
 TTTCTGAGTCTGACCACCTTCTGCTTACCAAGTGTGGGAGACTCTGATCCCTCTGCCCTGGCAGAATGG  
 CAGGGTAATCTGAGCCTTCTCACTCCTTACCCTAGCTGACCCCTCACCTCTCCCCCTCCCTTCTTGT  
 TTTGGGATTCAAGAAAATGCTGTCAGAGACTGTTATTTTATTAAAAATATAAGGCTTAAAAAA

## **FIGURE 158**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166
><subunit 1 of 1, 761 aa, 1 stop
><MW: 83574, pI: 6.78, NX(S/T): 4
MALPALGLDPWSLLGLFLFQLLQLLPTTAGGGGQGPMPRVRYAGDERRALSFFHQKGLO
DFDTLLLSDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSEAFKKKSNETQC
FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPAHKHTA
VLVDGMLYSGMTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHDASFVAAIPSTQVVYFFF
ETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLL
PADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPET
NPRPGSCSVGPSSDKALTFMKDHFIMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVM
YLGTTT GSLH KAVV SGDSS AHL VEE IQL FPD PEP VRNL QLAP TQG AVF VGFS GG VWR VPRAN
CSVYES CVDC VL ARDP HCA WDP E RT CCL L SAP NL NSW K QDM ERGN PEW ACAS GPM SRS LRP
QSRPQIIKEV LA VPNS ILEL PCPH LS AL AS YY WSH GP AA VPE AS STV YNG SLL I VQDG VGG
LYQC WA TENG FS YPV IS YW VD S QD QTL A LD P E L A G I P REH V KV PL TR VSG G A AL A QQ SY WP
HFVT VT VL FAL VLS GAL I I L VAS PL RAL RARG KV QGC ET LRP GEKA PL SRE QHL QSP KEC RT
SAS D VD A DN NCLG TEVA
```

**Signal peptide:**

amino acids 1-30

**Transmembrane domains:**

amino acids 136-156, 222-247, 474-490, 685-704

## **FIGURE 159**

AGGGTCCCTTAGCCGGCGCAGGGCGCGAGCCCAGGCTGAGATCCGCGGCTCCGTAGAAG  
**TGAGC****ATG**GCTGGCAGCGAGTGCTTCTCTAGTGGCTTCCTCTCCCTGGGGCCTGCTC  
 TCAGAGGCTGCCAAATCCTGACAATATCTACAGTAGGTGGAAGCATTATCTACTGATGGA  
 CGGGTTCTCAGATTCTCAAGATCACGGTCATAATGTCACCATGCTAACCAAAAGAG  
 GTCCTTTATGCCAGATTTAAAAGGAAGAAAATCATATCAAGTTATCAGTTGGCTTGCA  
 CCTGAAGATCATCAAAGAGAATTAAAAAGAGTTGATTCTTCTGGAAGAAACTTTAGG  
 TGGCAGAGGAAAATTGAAAACCTTAAATGTTCTAGAATACTTGGCGTTGCAGTGCAGTC  
 ATTTTTAAATAGAAAGGATATCATGGATTCCCTAAAGAATGAGAACCTCGACATGGTGATA  
 GTTGAACACTTTGACTACTGTCCTTCCTGATTGCTGAGAAGCTGGGAAGCCATTGTGGC  
 CATTCTTCCACTTCATTGGCTCTTGAATTGGCTACCAATCCCCTTGTCTATGTC  
 CAGTATTCCGTTCTGCTGACTGATCACATGGACTTCTGGGCCGAGTGAAGAATTTCTG  
 ATGTTCTTAGTTCTGCAGGAGGCAACAGCACATGCAGTCTACATTGACAAACACCATCAA  
 GGAACATTCACAGAAGGCTCTAGGCCAGTTGCTCATCTCTACTGAAAGCAGAGTTGT  
 GGTCATTAACCTGACTTGCCTTGATTTGCTCGACCTCTGCTTCCAACACTGTTTAT  
 GTTGGAGGCTTGATGGAAAAACCTATTAAACCAGTACCAAGACTGGAGAACATTGCTTGC  
 CAAGTTGGGACTCTGGTTTGCCTTGACCTGGCTCCATGGTAACACCTGTCAGA  
 ATCCGAAATCTCAAGGAGATGAACAATGCCTTGCTCACCTACCCCAAGGGGTGATATGG  
 AAGTGTCACTGTTCTCATTGGCCAAAGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGA  
 CTGGCTTCTCAGAGTGACCTCCTGGCTACCCAAGCATCCGTCTGTTGTCACCCACGGCG  
 GGCAGAATAGCATATGGAGGCCATCCAGCATGGTGTGCCATGGTGGGATCCCTCTCTT  
 GGAGACCTGAAACATGGTCCGAGTAGAAGCCAAAAGTTGGTGTGTTCTATTGAGTT  
 AAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGAT  
 ACAAGTCCGGCAGTGGCTGCCAGTGTCACTCCTGCGCTCCACCCGCTCAGCCCCACACAG  
 CGGCTGGTGGCTGGATTGACCACGTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTA  
 TGTCTTCAGCAGCCCTGGCATGAGCAGTACCTGTTGACGTTTGTGTTCTGCTGGGC  
 TCACTCTGGGACTCTATGGCTTGAGCTGCTGGCATGGCTGTCTGGTGGCTGCGT  
 GGGGCCAGAAAGGTGAAGGAGACA**TAA**GGCCAGGTGCGCCTGGGGGTCTGTTGGTGG  
 GCGATGTCAACCATTCTAGGGAGCTTCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTC  
 TAGTTATCTCCTGTTCTTGAGAACAGGAAAATGCCAAAATCATCCTTCCACTTGC  
 TAATTGCTACAAATTCACTCCTACTAGCTCCTGCCTGCTAGCAGAAATCTTCCAGCCT  
 CTTGCTCCTTGTGCTGCCATCAGCAAGGGCTATGCTGTGATTCTGCTCTGAGTGACTTG  
 GACCACTGACCTCAGATTCCAGCCTAAAATCCACCTCCTCTCATGCGCCTCTCCGAA  
 TCACACCCTGACTCTCCAGCCTCCATGTCAGACCTAGTCAGCCTCTCACTCCTGCC  
 TACTATCTATCATGGAATAACATCCAAGAAAGACACCTGCATATTCTTCAGTTCTGTT  
 TGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTCA  
 CGGACACAGGCTCACAGGTCTCCACATTGGTCCCTGTCTGGTCCCCACAGTGAGCTC  
 TCTTGGCTGAGCAGGCATGGAGACTGTAGGTTCCAGATTCTGAAAATAAAAGTTACA  
 GCGTTATCTCTCCCCAACCTCACTAA

## **FIGURE 160**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169
><subunit 1 of 1, 523 aa, 1 stop
><MW: 59581, pI: 8.68, NX(S/T): 1
MAGQRVLLLGVFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTMLNHKRGPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFFLEETLGGRGKFENLLNVLEYLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIPLSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLKAELWFINSDFAFDFARPLLPNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTLSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPVMVGIPLFQGDQOPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQYLFDFVFVFLGLTLGTLWLCGKLLGMAVWWLRGARKVKET
```

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 483-504

## **FIGURE 161**

GGGCTGTTGATTGTGGGGATTTGAAGAGAGGAGGAATAGGAGGAAGGGGTTGAGGGGCT  
 GCCTCTGGCATATGCACACACTCACACATTCTGTACACCCGTACACACACATACCATGTT  
 CTCCATCCCCCAGGTCCAGCCCTCAGTGTCTGCCATCCAGCAGGGCTACCCCTGAAGCTCT  
 GGCTGCAGCCCTCCCCTCAGTGGGCAGGCGGCTTCATCCCTCCTTCTCTCCAAAGGCCA  
 ACTGCTGTCAGTGCATGCTGCCAAGGAGGAGGAACTGCAGTGACAGCAGGAGTAAGAGT  
 GGGAGGCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGTTCAGCGAGCCTAGAGAGGGC  
 AGACTATCAGGGTGCCGGTGGAGAATCCAGGGAGAGGAGCGGAAACAGAACAGAGAGGGCAGA  
 AGACCGGGGCACTTGTGGGTTGCAGAGCCCTCAGCC**ATG**TGGGAGCCAAGCCACACTGGC  
 TACCAAGGTCCCCTACACAGTCCGGCTGCCCTGGTTCTGGTGCTTCTGCCCTGGGGC  
 GGGTGGGCCAGGAGGGTCAGAGCCCCTGCTGGAGGGGAGTGCCTGGTGGTCTGTGA  
 GCCTGGCCGAGCTGCTGCAGGGGGCCCGGGGAGCAGCCCTGGGAGAGGCACCCCTGGC  
 GAGTGGCATTGCTGCGGTCCGAAGCCACCACCATGAGCCAGCAGGGAAACCGGCAATGGC  
 ACCAGTGGGGCCATCTACTCGACCAGGTCTGGTGAACCGAGGGCGGTGGCTTGACCGGGC  
 CTCTGGCTCCTCGTAGCCCTGTCCGGGTGTCAGCTCCGGTTCCATGTGGTGAAGG  
 TGTACAACCGCCAAACTGTCCAGGTGAGCCTGATGCTGAACACGTGGCCTGTATCTCAGCC  
 TTTGCCAATGATCCTGACGTGACCCGGAGGCAGCCACCAGCTCTGTGCTACTGCCCTGGA  
 CCCTGGGACCGAGTGTCTGCGCCTGCGTCGGGAAATCTACTGGTGGTGGAAATACT  
 CAAGTTCTGGCTTCCATCTTCCCTCTC**TGA**GGACCCAAGTCTTCAAGCACAAGAAT  
 CCAGCCCTGACAACCTTCTTCTGCCCTCTTGCATGGCACCTGTGCCAAACACCCAAGTTAA  
 GAGAAGAGTAGAGCTGTCATCTCCAGACCAGGCCTTCCACCCACCCACCCAGTTACC  
 CTCCCAGCCACCTGCTGCATCTGTTCTGCCTGCAGCCCTAGGATCAGGGCAAGGTTGGCA  
 AGAAGGAAGATCTGCACTACTTGCCTCTGCTCCTCCGGTCCCCACCCAGCTTCC  
 GCTCAATGCTGATCAGGGACAGGTGGCGAGGTGAGCCTGACAGGCCACAGGAGGCCAG  
 ATGGACAAGCCTCAGCGTACCCCTGCAGGCTTCTCCTGTGAGGAAAGCCAGCATCACGGATC  
 TCAGCCAGCACCCTGCAAGCTGAGCCAGCACCCTGAGGCTAGGGTGGGAGGCTCAGCCAC  
 AGGCAGAAGGGTGGGAAGGGCTGGAGTCTGTTCTGGTGGAGGAAGGAAGGAGGGTGTATTG  
 TCTAGACTGAACATGGTACACATTCTGCATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCT  
 GGCTGTCTTCTATGCTGGATCCCAGATGGACTCTGCCCTTACCTCCCCACCTGAGATTAG  
 GGTGAGTGTGTTGCTCTGGCTGAGAGCAGAGCTGAGAGCAGGTATACAGAGCTGGAAGTGG  
 ACCATGGAAAACATCGATAACCCTGACATCCTCTGCTTGGCACCTCTGAAACTGCTCCAC  
 CTTTGAAGTTGAACCTTACTGCTCCACACTCTGACTGCTGCCTCCTCCTCCAGCTCTC  
 TCACTGAGTTATCTTCACTGTACCTGTTCCAGCATATCCCCACTATCTCTTCTCTGAT  
 CTGTGCTGTCTATTCTCCTCTAGGCTTCTATTACCTGGGATTCCATGATTCAATTCTT  
 CAGACCCCTCTGCCAGTATGCTAAACCCCTCTCTCTTCTTATCCCCTGTCCTCATT  
 GGCCCAGCCTGGATGAATCTATCAAATAAAACAACAGAGCTGAGAGCAGGTATACAGAGCTGGAAGTGG  
 AGAATTACTAAGGAGAAGATGCCCTGGAGTTGGATCAGGTACAGGTACAAGTAGGTA  
 TGTTGCAGAGGAAAATAATCAAACGTATACTAAAATTAAAAA

## **FIGURE 162**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180
><subunit 1 of 1, 205 aa, 1 stop
><MW: 21521, pI: 7.07, NX(S/T): 1
MLGAKPHWLPGPLHSPGLPLVLLVLLALGAGWAQEGSEPVLLEGECLVVCEPGRAAAGGPGGA
ALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVY
SFRFHVVVKVYNRQTVQVSLMLNTWPVISAFAANDPDVTREAATSSVLLPLDPGDRVSLRLRRG
NLLGGWKYSSFSGFLIFPL
```

**Signal peptide:**

amino acids 1-32

## **FIGURE 163**

GCTTTCTCGGCCACCACTGGCCGCCGGCCGCAGCTCCAGGTGTCCTAGCCGCCAGC  
 CTCGACGCCGTCCGGGACCCCTGTGCTCTGCGCGAAGCCCTGGCCCCGGGGCCGGGCAT  
 GGGCAGGGCGCGGGTGAAGCGCTTCCCGCGGGCCGTGACTGGCAGGCTCAGGCC**AT**  
**GAAGACCCTCATAGCCGCCTACTCCGGGTCTGCGCGAGCGTCAGGCCGAGGCTGACC**  
 GGAGCCAGCGCTCTCACGGAGGACCTGCCTGTCGCGAGGGCTGGAGATGGGCACT  
 GGATCCAGCATTCTCCGCCCTCCAGGACCTCTCTGTCACCTGGCTCAATAGGTCAA  
 GGTGGAAAAGCAGCTACAGGTATCTCAGTGCTCCAGTGGCTCTGTCCTCCTGTACTGG  
 GAGTGGCCTGCAGTGCCATCCTCATGTACATATTCTGCACTGATTGCTGGCTATCGCTGTG  
 CTCTACTTCACTTGGCTGGTGTGACTGGAACACACCCAAGAAAGGTGGCAGGAGGTACA  
 GTGGGTCCGAAACTGGGCTGTGGCGCTACTTCGAGACTACTTCCCATTCCAGCTGGTGA  
 AGACACACAAACCTGCTGACCACAGGAACATATATTTGGATACCACCCCCATGGTATCATG  
 GGCCTGGGTGCCTCTGCAACTTCAGCACAGAGGCCACAGAAGTGAGCAAGAAGTCCCAGG  
 CATACGGCCTTACCTGGCTACACTGGCAGGCAACTCCGAATGCCGTGTTGAGGGAGTACC  
 TGATGTCTGGAGGTATCTGCCCTGTCAGCCGGACACCATAGACTATTGCTTCAAAGAAT  
 GGGAGTGGCAATGCTATCATCGTGGTCGGGGTGCAGCTGAGTCTCTGAGCTCCATGCC  
 TGGCAAGAACATGCAGTCACCCCTGGGAACCGCAAGGGCTTGTGAAACTGGCCTGCGTCATG  
 GAGCTGACCTGGTCCCACACTCCTTGGAGAGAACATGAAGTGTACAAGCAGGTGATCTC  
 GAGGAGGGCTCCTGGGCCGATGGTCCAGAAGAACATACATTGGTTGCC  
 ATGCATCTCCATGGTCAGGCCTTCTCCTCCGACACCTGGGGCTGGTGCCTACTCCA  
 AGCCCATCACCACACTGTTGGAGAGCCCATCACCACCCAAAGCTGGAGCACCCAAACCCAG  
 CAAGACATCGACCTGTACACACCATGTACATGGAGGCCCTGGTAAGCTCTCGACAAGCA  
 CAAGACCAAGTCGGCCTCCGGAGACTGAGGTCCGGAGGTGAAC**TGA****GCCAGCCTCGGG**  
 GCCAATTCCCTGGAGGAACCAGCTGCAAATCACTTTTGTCTGTAATTGGAAAGTGTCA  
 TGGGTGCTGTGGTTATTAAAAGAAATTATAACAATTGCTAAACCAAAAAAAA  
 AAAAAAAA  
 AAAAAAAA

## **FIGURE 164**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184
><subunit 1 of 1, 388 aa, 1 stop
><MW: 43831, pI: 9.64, NX(S/T): 3
MKTLLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNR
KVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLIAVLYFTWLVDWNTPKGGRRS
QWVRNWAHWRYFRDYFPIQLVKTHNLLTRNYIFGYHPHGIMGLGAFCNFSTEATEVSKKFP
GIRPYLATLAGNFRMPVLREYLMGGICPVSRTIDYLLSKNGSGNAIIVVGGAAESLSSM
PGKNAVTLRNRKGFKLALRGADLVPIYSFGENEVYKQVIFEEGSWGRWVQKKFQKYIGFA
PCIFHGRGLFSSDTWGLVPYSKPITTVVGEPIТИPKLEHPTQQDIDLHYHTMYMEALVKLFDK
HKTGFGLPETEVLEVN
```

**Important features of the protein:**

**Transmembrane domain:**

amino acids 76-97

**N-glycosylation sites.**

amino acids 60-63, 173-176, 228-231

**N-myristoylation sites.**

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-  
245, 318-323, 378-383

## **FIGURE 165**

GGGCGCGGGGATGGGGCCGGGGCGGGCGCCGCACTCGCTGAGGCCCGACGCAGGGCCGGCCGGCCA  
 GGGCGAGGAGCGCGGCGGCCAGAGCAGGGCGGGAGGCACGCCGCGACGAGCAGGTGGCG  
 GCGGCTGCAGGCTTGTCCAGCCGAAGCCCTGAGGGCAGCTGTTCCCACTGGCTCTGCTGACCTTGCGCTTGGA  
 CGGCTGTCTCAGCGAGGGCGGTGCACCCGCTCTGAGCAGCGCC**ATG**GGCCTGCTGGCCTTCCTGAAGACCCA  
 GTTCGTGCTGCACCTGCTGGTCGGCTTGTCTCGTGGTAGTGGCTGGTCATCAACTCGTCCAGCTGTGCAC  
 GCTGGCGCTCTGCCGGTCAGCAAGCAGCTTACCGCCGCTCAACTGCCGCTGCCACTCACTCTGGAGCCA  
 ACTGGTCATGCTGCTGGAGTGGTGGCTGCACGGAGTGTACACTGTTACGGACCAGGCCACGGTAGAGCGCTT  
 TGGGAAGGAGCACCGCAGTCATCATCCTCAACCACAATTGAGATCGACTTCCTCTGTGGGTGGACCATGTGTGA  
 GCGCTTCGGAGTGTGGGGAGCTCCAAGGTCTCGCTAAGAAGGAGCTGCTTACCGTCCCCCTCATGGCTGGAC  
 GTGGTACTTTCTGGAGATTGTGTTCTGCAAGCGGAAGTGGGAGGAGGACCGGGACACCGTGGTGAAGGGCTGAG  
 GCGCCTGCGACTACCCCGAGTACATGTGGTTCTCTGTACTGCGAGGGGACCGCCTCACGGAGACCAAGCA  
 CCGCGTTAGCATGGAGGTGGCGGCTGCTAAGGGCTTCTGCTCAAGTACCACTGCTGCCGCGGACCAAGGG  
 CTTCACCACCGCAGTCAGTGCCTCCGGGGACAGTCGAGCTGTCTATGATGTAACCTGAACATTCAAGAGGAAA  
 CAAGAACCGTCCCTGCTGGGATCCTCTACGGGAAGAAGTACGAGGGGACATGTGCGTGAGGAGATTTCTCT  
 GGAAGACATCCCGCTGGATGAAAGGAAGCAGCTCAGTGGCTCATAAACTGTACCAAGGAGAAGGACCGCCTCCA  
 GGAGATATATAATCAGAACGGGATGTTCCAGGGAGCAGTTAACGCTGCCGGAGGCCGTGGACCCCTCTGAA  
 CTTCCCTGCTGGCCACCATCTCTGTCTCCCCTTCTCAGTTGTCTGGCGCTTGGCCAGCGGATCACC  
 TCTCCTGATCCTGACTTTCTGGGTTGTGGGAGCAGCTCCTTGGAGTTCGCAACTGATAGGAGAACGCT  
 TGAACTGGGAGGTGGAGATTGCA**TG**GCTGAGATGGCATCACTGTACTCCAGCTAGGCAACAGAGCAAGACT  
 CAGTCTAAAAAAAAAAAAACAAAAACCCAGAAATTCTGGAGTTGAACGTGTAGTTACTGACATGAAAA  
 ATTCACTAGAGGCTGAACAGCAGATTGAGCAGGGAGAAAAATCAGCAAGCTGAAGATGGTACCTTGAGATT  
 TTTCAGGCTAATGAAAAAATGAAGGAAAATTAAACAGCCTCAGAGACCCATGGTGCACCGTCACACAAATCAA  
 CATATGCATGATGAGAGTCCAGAAGGAGAGGAGAAAGGGTCAGAAAGAATGCCACAAGCTGATGAAAAACA  
 GTAACCTACCCACTCAGGAAGCTCAGTGAACCTCAATGAGGATGAATATCAGAGATCCACACCTAGATATTCAT  
 AATCAAAGTGTCAAATGACAAAGAATCTGAAAGCAGCAAGAGATGAGCAACTTATCTGTTCAAAGGATTTG  
 ATCAGATTAACAGCTCATTCTCTCAGAAATCATGGGAGGCCAGGAGATAGTGGGATGAACACTGTTGAAGGCAA  
 AACCTCAACTGTAATTATTGGACTTTGAGTCTTAGATGGCCTGACCTCTTGCTTCAGGGACAGTTTCA  
 ATTTAATCCCTAATAACAATTAGTCAGCTTCTTGACCTGTAGGAAGGCCGTCTTAGGCCGGCACAGTGGC  
 TTACACCTGTAATCCAGCAGCTTGGGAGGCCAGACGGGTGGATCATTGGGTCAGGCTGATCTCAAACCTCT  
 GAGTTCAGGTGATCTGCCGCCCTCAGCCTCCAAAGTGTGATTGCAAGGCGTGAAGCCACTGCGCTGGCGGA  
 ATTTCTTTAAGGCTGAATGATGGGGCCAGGCACGATGGCTCACGCCGTGATCCAAGTAGCTTGATTGTA  
 AACATGCACCACCATGCCTGGCTAATTTGTATTTAGTAGAGACGTGTTAGCCAGGCTGGCTCGATCTCCT  
 GACCTCAAGTGACCACTGCCCTCAGCCTCCAAAGTACTGGGATTACAGGCGTGAAGCCACTGTCGCTGGCCTTGA  
 GCATCTGTGATGTGTTATTGCCATTGTATATCTCTATCTTGGGAAATGTCTGTTCAAGTCTTGT  
 CCTTTTAAATTTTATTATTATTATTGAGACAGGGCTTGTTCTGTTGCCAGGCTGGAGTA  
 CAGTGGCACAGTCTGGCTACTGCAGCCTCGACCTCCTGGCTGAGTGTGATCCTCCACCTCAGCCTCCCTGT  
 AGCTGTATTTTGATTTGTATTTGTAGCTGAGTTTGATTTTGATTTGTGGAGACAGCATTTCACCATGA  
 TGCCCAAGGCTGGCTTGAACTCCTGAGCTCAAGTGTGATCTGCCCTGCTCAGCCTCCAAAGTGTGGGATTACAGA  
 CATGAGGCCACTGCACCTGGCAAACCTCCAAAATTCAACACACACACACACACACACACACACACACACACAC  
 GAGGGGCCGGGTGTGGCCCAAACCTACCAAGGGAGACTGAAGTGGGAGGATCGCTGGCATGAGAAGTCGAGGCTG  
 CAGTGAGTCGAGGTTGTGCGACTGCATTCCAGCCTGGACAACAGAGTGAGACCCGTCTC

## **FIGURE 166**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213
><subunit 1 of 1, 368 aa, 1 stop
><MW: 42550, pI: 9.11, NX(S/T): 1
MGLLAFLKTQFVLHLLVGFVFVSGLVINFVQLCTLALWPVSKQLYRRLNCRLAYSLWSQLV
MLLEWWSCTECTLFTDQATVERFGKEHAVIILHNHNFEDFLCGWTMCERFGVLGSSKVLAKK
ELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHR
VSMEVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAAVYDVTLNFRGNKNPSLLGILYGKK
YEADMCVRRFPLEDIPDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLLN
FLSWATILLSPLFASFVLGVFASGSPLLILTFLGFVGAASFGVRRLIGESLEPGRWRLQ
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**Transmembrane domains:**

amino acids 307-323, 335-352

**Tyrosine kinase phosphorylation sites.**

amino acids 160-168, 161-169

**FIGURE 167**

GATATTCTTATTTAAGAACCTGAAGTACTATGCATCACTCCCTCCAATGTCCTGGGC  
GCCACCAGGCATATTCATCTTGTGTGTTCTTTGCTTAGCACTGGGCACCTCTT  
GCTTATTCTTGCTGGTAGGAAAGGGGCTCAGTTGTCTGTGGGTTGGTGGCAGGCAGGCCG  
GCTTACGCCTGATAACGCCCTGGGTTAGAAGGGAAAGGAAAGATAAACTTTATACAAATGGG  
GATAGCTGGGTCTGAGACCTGCTCCTCAGTAAAATTCTGGATCTGCCTATACCTCTT  
TTCTCTAACCTGGCATACCCTGCTAAAGCCTCTCAGGGCTCTCTGTTCTAGGATCAA  
AGTATTAGAGCTACAAGAGCCCTCATGGTCTGGCCCTGCCCCCTGGCCAGCTCATTGT  
ACATGTGGTGTCTCTGCTGTTCTGTAATGTGGTATGCCATGGGTCTTGCACAAGCCT  
TTCCCTTTGGCTGGACACTGTCCCTGCCCTCCCCCATACTCTCCTACTTAATATGTAGTC  
ATCCTGCAGATTCAATTCTAACATCATTCTCCAGGGATCCTGGCCTGACAGAATCTCAT  
CTTGTAAATGCTCTCATAAGACCACTTGTCCCTTGCAGCACTGCCACTCAGTTGTA  
TCTTATGTGCGTTGTGGTTGTATGGGTGTCTGTTCCCAGAATGCCAGCTTGAGC  
TGCCTGAGGGTCAAGGGCATTGCTGTGCCAGGTATAGCCTACATGTGGTGGGTGCT  
CATTTTAGAGACTAAATGGAGGGAGATGAGGAAAGATTGAAATCTCAGTTCACCA  
GATGGTGTAGGGCCCAGCATTGTAATTACACAGTTGACTGTGCTTGTGAATTATCTGGGA  
TGCAGGTCTGATTCACTAGGCCAGGTGGCATCTCTAACAAACTCCCACGTGATGCTGA  
TGCTGGTCCTATGAACATATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGCATGGC  
TCACACCTATGATCCCAGCACTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATT  
TCAAGACTAGCCTGGCCAACATGGTGGAACCCATCTGTACTAAAAATACACAAATTAGCTG  
GGCATGGTGGCACATGCCCTGTTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTG  
AACCTGGGAGGGCGGAGGTTGCAGTGAGCCAGTCAGGCCACTGTATTCCAACCAGGGTGAC  
AGAGTGAGACTCTATGTCCAAAAAAAAAAAAAA

## **FIGURE 168**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234
><subunit 1 of 1, 143 aa, 1 stop
><MW: 15624, pI: 9.58, NX(S/T): 0
MHHSILQCPGAATRHIHLCVCFSFALALGHFLLISLVGKGLSLSGVGGRQAGLRLIRPWVRR
EGKINFYTNGDSWGLRPASSVKFLGSAYTFFSLTWHTLLKASQGFSLFLGSKYLELQEPSWS
GPCPPGQLHCTCGVLLSFL
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-28

## **FIGURE 169**

GGCTGGACTGGAACCTCCTGGTCCAAGTGATCCACCCGCCTCAGCCTCCAAGGTGCTGTGA  
 TTATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACTTTCACTAAGGAACTAAAAAGCCAC  
 AGGAGTTGAAC TGCTAGGATTCTGACT**ATG**CTGTGGTGGCTAGTGCTCCTACTCCTACCTAC  
 ATTAAAATCTGTTTTGTTCTTGTAACTAGCCTTACCTTCCTAACACAGAGGATCTGT  
 CACTGTGGCTCTGCCAAACCTGACCTCACTCTGGAACGAGAACAGAGGTTCTACCCAC  
 ACCGCCCCCTCGAAGCCGGGACAGCCTCACCTGCTGCCCTCGCTGGAGCAGTGCCCTC  
 ACCAACTGTCTCACGTCTGGAGGCAGTGACTCGGGCAGTGAGGTAGCTGAGCCTCTGGTA  
 GCTGCGGCTTCAAGGTGGCCTGCCCTGGCGTAGAAGGGAT**TGA**CAAGCCGAAGATT  
 CATAGGCGATGGCTCCACTGCCAGGCATCAGCCTGCTGTAGTCATCAGGCCCTGGGG  
 CCAGGACGGGCCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCGCCAT  
 CTAACCTTTCATGTCTGCACATCACCTGATCCATGGCTAATCTGAACCTGTCCCCAAGG  
 AACCCAGAGCTTGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTT  
 TATGTGACAGGACTTGACATTCTCCTGAAACATGAGGGAACGCCGGAGGAAAGCAAAGTGGCA  
 GGGAAAGGAACATTGTGCCAAATTATGGGTCAAGAAAAGATGGAGGTGTGGTTATCACAAGGC  
 ATCGAGTCTCCTGCATTCACTGGACATGTGGGGAAAGGGCTGCCATGGCGCATGACACACT  
 CGGGACTCACCTCTGGGCCATCAGACAGCCGTTCCGCCCGATCCACGTACAGCTGCTG  
 AAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAATCTGCGATCACCAG  
 CCAGGGGCAGCCGTCTGGGAGGAGCAAGCAAAGTGACCATTCTCCTCCCCCTTCCCTC  
 TGAGAGGCCCTCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGCTAATG  
 GCTCAGTGTGGCCCAGGAGGTCAAGAACGGCTGAGAGCTGATCAGAACGGCTGCTGTGCG  
 AACACGGAAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGGCT  
 CAATTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGG  
 TCAAATGATCTCCAAGGGCCCTATAACCCAGGAGACTTGATTTGAATTGAAACCCCAA  
 TCCAAACCTAAGAACCCAGGTGCATTAAGAACATCAGTTATTGCCGGGTGTGGTGGCTGTAATG  
 CCAACATTGGGAGGCCGAGGCCGGTAGATCACCTGAGGTCAAGACAGCAGGCTG  
 GCCAACATGGTGAACCCCTGTCTACTAAAAATACAAAAAAACTAGCCAGGCATGGTGG  
 GTGTGCCCTGTATCCCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGG  
 GAAGGAGGCTGAGACAGGAGAATCACTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGA  
 AAAAATAAAAAAGAATTATGGTTATTGTAA

## **FIGURE 170**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277
><subunit 1 of 1, 109 aa, 1 stop
><MW: 11822, pI: 8.63, NX(S/T): 0
MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWPKPDLHSGTRTEVSTHTVPSKPGTA
SPCWPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRD
```

**Signal peptide:**

amino acids 1-15

**FIGURE 171**

GCGGGCCCGCGAGTCCGAGACCTGTCCCAGGAGCTCCAGCTCACGTGACCTGTCACTGCCTC  
CCGCCGCTCCTGCCCGGCCATGACCCAGCCGGTCCCCCGCTCTCCGTGCCGCCGCGCT  
GGCCCTGGCTCAGCCGACTGGCGCCCTCGCCACTGGCCTCTCCTGGGGAGGCGGT  
GCCCCCCATGGCGAGGCCGGCGAGAGCAGTGCCTGCTTCCCCCGAGGAACAGCCGCCTGTGG  
CAGTATCTTCTGAGCCGCTCCATGCAGGGAGCACCCGGCGCTGCGAACCTGAGGCTGCTGAC  
CCTGGAGCAGCCGCAGGGGATTCTATGATGACCTGCGAGCAGGCCAGCTCTGGCCAACC  
TGGCGCGGCTCATCCAGGCCAAGAAGGCCGCTGGACCTGGCACCTCACGGCTACTCCGCC  
CTGGCCCTGGCCCTGGCGCTGCCCGGGACGGCGCGTGGTGACCTGCGAGGTGGACGCGCA  
GCCCGGGAGCTGGACGGCCCTGTGGAGGCAGGCCGAGGCCGAGCACAAAGATCGACCTCC  
GGCTGAAGCCCGCTTGGAGACCCCTGGACGAGCTGCTGGCGCGGGCAGGCCGACCTTC  
GACGTGGCGTGGTGGATGCGGACAAGGAGAACTGCTCCGCCTACTACGAGCGCTGCCTGCA  
GCTGCTGCGACCCGGAGGCATCCTGCCGTCCAGAGTCCTGTGGCGCGGGAAAGGTGCTGC  
AACCTCCGAAAGGGACGTGGCGCCGAGTGTGCGAAACCTAAACGAACGCATCCGGCGG  
GACGTCAAGGTCTACATCAGCCTCTGCCCTGGCGATGGACTCACCTTGGCCTCAAGAT  
CTAGGGCTGGCCCTAGTGAGTGGCTCGAGGGAGGGTTGCCTGGAACCCCAGGAATTGAC  
CCTGAGTTAAATTGAAAATAGTGGGCTGGGACACAAAAAA

## **FIGURE 172**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282
><subunit 1 of 1, 262 aa, 1 stop
><MW: 28809, pI: 8.80, NX(S/T): 1
MTQPVPRLSVPAALALGSAALGAAFATGLFLGRRCPWRGRREQCLLPPEDSRLWQYLLSRS
MREHPALRSLLTLEQPQGDMMTCEQAQLLANLARLIQAKKALDLGTFTGYSALALALAL
PADGRVVTCEVDAQPPELGRPLWRQAEAEHKIDLRLKPALETLDDELLAAGEAGTFDVAVVDA
DKENCSAYYERCLQLLRPGGILAVLRVLWRGKVLQPPKGDVAAECVRNLNERIRRDVRVYIS
LLPLGDGLTLAFKI
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**Transmembrane domains:**

amino acids 8-30, 109-130

**N-glycosylation site.**

amino acids 190-193

**Tyrosine kinase phosphorylation site.**

amino acids 238-246

**N-myristoylation sites.**

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

**Amidation sites.**

amino acids 31-34, 39-42

## **FIGURE 173**

CCGCCGCCGCAGCCGTACCGCCGCTGCAGCCGCTTCCGGCCTGGCCTTCGCCGTCA  
**GCATG**CCACACGCCCTCAAGCCCCGGGACTTGGTGTGCTAAGATGAAGGGCTACCCCTCAC  
 TGGCCTGCCAGGATCGACGACATCGCGGATGGCGCCGTGAAGCCCCCACCAACAAGTACCC  
 CATCTTTCTTGGCACACACGAAACAGCCTCCTGGGACCCAAGGACCTGTTCCCCTACG  
 ACAAAATGTAAAGACAAGTACGGGAAGGCCAACAAAGAGGAAAGGCTTAATGAAGGGCTGTGG  
 GAGATCCAGAACAAACCCCCACGCCAGCTACAGC GCCCTCCGCCAGTGAGCTCCTCCGACAG  
 CGAGGCCCCCGAGGCCAACCCCGCCAGGGCAGTGACGCTGACGAGGACATGAGGACCGGG  
 GGGTCATGGCCGTACAGCGTAACCGCCACAGCTGCCAGCGACAGGATGGAGAGCGACTCA  
 GACTCAGACAAGAGTAGCGACAAACAGTGGCCTGAAGAGGAAGACGCCCTGCGCTAAAGATGTC  
 GGTCTCGAAACGAGCCGAAAGGCCCTCAGCGACCTGGATCAGGCCAGCGTGTCCCCATCCG  
 AAGAGGAGAACTCGGAAAGCTCATCTGAGTCGGAGAAGACCCAGCGACCAGGACTTCACACCT  
 GAGAAGAAAGCAGCGGTCCGGCGCCACGGAGGGCCCTCTGGGGGGACGGAAAAAAAAGAA  
 GGCGCCGTAGCCTCCGACTCCGACTCCAAGGCCATTGGACGGGGCCAAGCCTGAGCCGG  
 TGGCCATGGCGCGTCTCCTCCTCTCTCTCTCTCTCCGACTCCGATGTG  
 TCTGTGAAGAAGCCTCCGAGGGGCAGGAAGCCAGCGGAGAAGCCTCTCCGAAGCCGCGAGG  
 GCGGAAACCGAAGCCTGAACGCCCTCCGTCCAGCTCCAGCAGTGACAGTGACAGCGACGAGG  
 TGGACCGCATCAGTGAGTGGAAAGCGGGGACGAGGCGCGAGGCGAGCTGGAGGCCCGG  
 CGCGCGAGAGCAGGAGGAGCTCGGGCGCTCGGGAGCAGGAGAAGGAGGAGAAGGA  
 GCGGAGGGCGCAGCGGGCCGACCGCGGGGAGGCTGAGCGGGGAGCGGGCAGCAGCGGGG  
 ACGAGCTCAGGGAGGACGATGAGCCGTCAAGAACGGGGACGCAAGGGCCGGGGCGGGG  
 CCCCCGTCTCCTCTGACTCCGAGGCCGAGCTGGAGAGAGAGGCCAAGAAATCAGC  
 GAAGAACGCCAGTCCTCAAGCACAGAGCCGCCAGGAAACCTGGCCAGAAGGAGAAGAGAG  
 TGCGGCCCGAGGAGAACACAAGCCAAGCCGTGAAGGTGGAGCGGACCCGGAAGCGGTCC  
 GAGGGCTTCGATGGACAGGAAGGTAGAGAAGAACAGGCCCTCCGTGGAGGAGAACG  
 GCAGAACGCTGCACAGTGAGATCAAGTTGGCTAAAGGTGACAGGCCGGACGTGAAGAGGT  
 GCCTGAATGCCCTAGAGGAGCTGGGAACCCCTGAGGTGACCTCTCAGATCCTCCAGAAGAAC  
 ACAGACGTGGTGGCCACCTTGAGAACAGATTGCGCTTACAAAGCGAACAGGACGTAATGGA  
 GAAGGCAGCAGAACAGTCTATACCCGGCTCAAGTCGGGGCTCTCGGCCAAAGATCGAGGC  
 TGCAGAAAGTGAACAAGGCTGGGATGGAGAACGGAGAACGGCGAGGAGAACGCTGGCC  
 GAGCTGGCCGGGGAGGAGGCCCCCAGGAGAACGGCGAGGACAAGCCCAGCACCGATCTC  
 AGCCCCAGTGAATGGCGAGGCCACATCACAGAACGGGGAGAGCGCAGAGGACAAGGAGCAG  
 AGGAGGGTGGACTCGGAGGAGGGCCAAGGTGTTGGCTCTGAAAGACCTGCACGACAGC  
 GTACGGGAGGGTCCGACCTGGACAGGCCCTGGAGCGACGGGAGCGAGGAGCGAGAGGGCAGC  
 GGGGGACTCGGAGGCCCTGGACGAGGAGAG**TGA**GCCGCGGGCAGCCAGGCCAGCCCC  
 CCGAGCTCAGGCTGCCCTCTCCTCCGGCTCGCAGGAGAGCAGAGCAGAGAACACTGTGGG  
 GAACGCTGTGCTGTTGTATTGTCCTGGGTTTTTCTGCTGCTAAATTCTGTGATT  
 TCCAACCAACATGAAATGACTATAACGGTTTTAATGA

**FIGURE 174**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286
><subunit 1 of 1, 671 aa, 1 stop
><MW: 74317, pI: 7.61, NX(S/T): 0
MPHAFKPGDLVFAKMKGYPHWPARIDDIADGAVKPPPNKYPIFFFTHETAFLGPKDLFPYD
KCKDKYGKPNKRKGFNEGLWEIQNNPHASYSAPPVSSSDSEAPEANPADGSDAEDDEDRG
VMAVTAVTATAASDRMESDSDKSSDNSGLRKTPALKMSVSKRARKASSLDQASVSPSE
EENSESSSESEKTSQDFTPEKKAAVRAPRRGPLGGRKKKKAPSASDSDKADSDGAKPEPV
AMARSASSSSSSSSSDSVVKPPRGRKPAEKPLPKPRGRKPAPPERPPSSSSDSDSDEV
DRISEWKRRDEARRRELEARRREQEEELRRLREQEKEEKERRERADRGEAERGSGGSGD
ELREDDEPVKKRGRKGRGRGPPSSDSEPEAELEREAKSAKKPQSSTEPARKPGQKEKRV
RPEEKQQAKPVKVERTRKRSEGFMDRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRC
LNALEELGTIQLQVTSQILQKNTDVVATLKKIRRYKANKDVMEMKAAEVYTRLKSRLGPKIEAV
QKVNKAGMEKEKAEEKLAGEELAGEEAPQEKAEDKPSTDLSAPVNGEATSQKGESAEDKEHE
EGRDSEEGPRCGSSEDLHDSVREGPDLLRPGSDRQERERARGDSEALDEES
```

**Signal peptide:**

amino acids 1-13

## FIGURE 175

GTTGGTTCTCTGGATCTCACCTTACCAACTGCAGATCTTGGGACTCATCAGCCTCAATAATTATATAAATTA  
 ACACCATTGAAAGAGAACATTGTTTCATC**ATGA**ATGCTAATAAAGATGAAAGACTTAAAGCCAGAACCAAGA  
 TTTCACCTTTCTGCTTGTGATGATGCTAACCATGACCATGTTGTTCTTCAGTCAGTGGCACTTGAAGCA  
 AAATATTCCAAGACTCAAGCTAACCTCAAAGACTTGCTGCTTCAAATAGCTGTATCCCTTTGGGTTCATC  
 AGAAGGACTGGATTTCAAACACTCTCTTAGATGAGGAAAGGGCAGGCTGCTCTGGGAGCCAAAGACACAT  
 CTTCTACTCAGTCTGGTTGACTTAAACAAAATTAAAGAAGATTATTGGCCTGCTGCAAAGGAACGGGTGGA  
 ATTATGTAAATTAGCTGGGAAAGATGCCAACATCAGAATGTGCAAATTTCATCAGAGTACTTCAGCCCTATAACAA  
 AACTCACATATATGTGTGGAACGGAGCATTTCATCCAATATGTGGGTATTGATCTTGGAGTCTAACAGGA  
 GGATATTATATTCAAACACTAGACACACATAATTGGAGTCTGGCAGACTGAAATGTCTTCGATCCTCAGCAGCC  
 TTTGCTCAGTAATGACAGATGAGTACCTCTACTCTGGAACAGCTCTGATTTCTTGGCAAAGATACTGCATT  
 CACTCGATCCCTGGGCCTACTCATGACCACCATACATCAGAACTGACATTTCAGAGCACTACTGGCTCAATGG  
 AGCAAAATTATTGGAACCTCTTACACAGACACCTACAATCCAGATGATGATAAAATATATTCTCTTCG  
 TGAATCATCTCAAGAAGGCAGTACCTCCGATAAAACCATCCTTCTCGAGTTGGAAAGAGTTGTAAGAATGATGT  
 AGGAGGACAACGCGCCTGATAAACAAAGTGGACGACTTTCTTAAGGCCAGACTGATTGCTCAATTCTGGAAAG  
 TGATGGGGCAGATACTTACTTGTGAGCTTCAAGATATTATTACTCCCCACAAGAGATGAAAGAAATCCTGT  
 AGTATATGGAGTCTTACTACAACCAGCTCCATCTCAAAGGCTCTGCTGTTGTGATAGCATGGCTGACAT  
 CAGAGCAGTTTAATGGTCCATATGCTCATAAGGAAAGTGCAGACCATCGTTGGGTGAGTATGATGGGAGAAT  
 TCCTTATCCACGCCCTGGTACATGTCAAAGCAAACCTATGACCCACTGATTAAGTCCACCCGAGATTTCAGA  
 TGATGTCATCAGTTCTAAAGCGGCACTCTGTGATGTATAAGTCCGTATAACCCAGTTGCAAGGAGGACAAACGTT  
 CAAGAGAATCAATGTGGATTACAGACTGACACAGATAGTGGGATCATGTCATTGCAAGAGATGGCAGTACGA  
 TGTAATGTTCTTGGAAACAGACATTGGAACTGTGCTCTCAAAGTTGTCAGCATTCAAAGGAAAGTGGAAATATGGA  
 AGAGGTAGTGTGGAGGAGTTGAGATATTCAAGCACTCATCAATCATCTTGAACATGGAATTGTCTCTGAAGCA  
 GCAACAATTGTACATTGGTCCCAGATGGATTAGTTCAGCTCTTGCACAGATGCGACACTATGGGAAAGC  
 TTGCGCAGACTGTGCTTGGCAGAGACCCCTACTGTGCTGGATGGAAATGCGATGCTCTCGATATGCTCCTAC  
 TTCTAAAAGGAGAGCTAGCGCAAGATGTAAAATATGGCACCACATACCCAGTGTGCTGGACATCGAACAG  
 CATTAGTCATGAAACTGCTGATGAAAAGGTGATTTGGCATTGAATTAACTCAACCTTCTGGAAATGTATACC  
 TAAATCCAAACAGCAACTATTAAATGGTATATCAGAGGTAGGGGATGAGCATCGAGAGGAGTTGAAGCCGA  
 TGAAAGAATCATCAAAACGGAAATGGGCTACTGATTGCAAGTTGCAAGAAGAAGGATTCTGGGATGTTACTG  
 CAAAGCCCAGGAGCACACTTACATCCACACCAGTGAAGCTGACTTTGAATGTCATTGAGAAATGAACAGATGGA  
 AAATACCCAGAGGGCAGAGCATGAGGAGGGCAGGTCAAGGATCTATTGGCTGAGTCACGGTGGAGATAACAAAGA  
 CTACATCCAAATCCTAGCAGCCAAACTCAGCCTCGACCAGTACTGCGAACAGATGTCAGGAGGAGCG  
 GAGACAGAGAAACAAGGGGCCAAAGTGGAAAGCACATGCAAGGAAATGAAGAAGAAACGAAATCGAACATCA  
 CAGAGACCTGGATGAGCTCCCTAGAGCTGTAGCCAG**TAG**TTTCTACTTAATTAAAGAAAATCCTTAC  
 TATAAAACATTGCCCTCTGTTTGATATCCCTATAGTAATTCAATAATGCTCCATGGAGTTTGCTAAGG  
 CACAAGACAATACTGAAATAAGACAATATGTGATGAATATAAGAAAGGGAAAAATTATTGAACCAGTTT  
 CCAAGAACAAATCTGCACAAGCAAAGTATAAGAATTATCCTAAAAATAGGGGTTACAGTTGTAATGTTTA  
 TGTTTGGTAAATTATTGTCATGTAATAGTGTGAGCTAAGCAAGCCCGAATTGATAGTGTATAAGGT  
 GCTTTATCCCTCGAATGTCCATTAAGCATGGAATTACCATGTCAGTTGTGCTATGTTCTTATGAACAGATAT  
 CATTCCATTGAGAACAGCAGCTACCTGTGGTAGGGATAAGAGGTAGACACAAATTAAAGACAACCTCCATTATC  
 AACAGGAACATTCTCAGTGAGCCATTCACTCTGGAGAAATGGTATAGGAATTGGAGAGGTGCAATTCTTCTTC  
 TGGCCACTGGGGTAAATTAGTGTACTACAAACATTGATTTACTGAAAGGGCACTAATGTTCCCCCAGGATTCT  
 ATTGACTAGTCAGGAGTAACAGGTTACAGAGAGAAGTTGGGCTTAGTTAGTGTGTTTTAGAGTATATACTAA  
 GCTCTACAGGGACAGAACATGCTTAATAAAACTTTAATAAGATATGGGAAAATTTTAATAAAACAAGGAAAACA  
 TAATGATGTATAATGCATCTGATGGGAAGGCATGCAAGATGGGATTGTAGAAGACAGAAGGAAAGACAGCCAT  
 AAATTCTGGCTTGGGAAAATCATATCCCCATGAAAAGGAAGAACATCACAAATAAGTGGAGAGTAATGTA  
 TGGAGCTTTCACTAGGGTATAAGTAGCTGCCAATTGTAATTGATCTGTTAAAAAAATCTAGATTATAACA  
 AACTGCTAGCAAATCTGAGGAAACATAAAATTCTCTGAGAATCATAGGAAGAGTAGACATTATTATTAACC  
 AATGATATTCTCAGTATATATTCTCTTTAAAAAAATTATTCATACTCTGTATATTATTCTTTACTGC  
 CTTTATTCTCCTGTATATTGGATTTGTGATTATATTGAGTGAATAGGAGAAAACAATATAACACACAGA  
 GAATTAAGAAAATGACATTCTGGGAGTGGGATATATTGTTGAATAACAGAACGAGTGTAAAATTAAAC  
 AACGGAAAGGGTTAAATTAAACTCTTGACATCTCACTCAACCTTCTCATTGCTGAGTTAATCTGTTGAATT  
 GTAGTATTGTTTGTAAATTAAACAATAAGCCTGCTACATGT

**FIGURE 176**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883
><subunit 1 of 1, 777 aa, 1 stop
><MW: 89651, pI: 7.97, NX(S/T): 3
MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNI PRLKLTYKDLLLNSCIPFL
GSSEGLDFQTLLLDEERGRLLLGAKDHFLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDA
NTECANFIRVILQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRLKCPFD
PQQPFASVMTDEYL YSGTASDFLGKDTAFTRSLGPTHDH YIRTDISEHYWLNGAKFIGTFF
IPDTYNPDDD KIYFFFRESSQEGSTS DKTILSRVGRVCKNDVGGQRSLINKWTTFLKARLIC
SIPGSDGADTYFDELQDIYLLPTRDERNPV VYGVFTTSSIFKGSAVCVYSMADIRAVFNGP
YAHKESADHRWVQYDGRIPYPRPGTCPSKYDPLIKSTRDFPDDVISFIKRHSVMYKSVYPV
AGGPTFKRINV DYRLTQIVVDH VIAEDGQYDVMFLGTDIGTVLKVV SISKEKWNMEEV LEE
LQIFKHSSII LNME SLKQQQLYIGSRDGLVQLSLHRCDTY GKACADC CLARDPYCAWDGNA
CSRYAPTSKRRARRQDV KYGDPI TQCWDIEDSIS HETADEKV IFGIEFNSTFLECIPKSQQA
TIKWYIQRSGDEHREELKPDERII KTEY GLLIRSLQKKD SGMYY CKAQEHTFIHTIVKLTLN
VIENEQMENT QRAEHEEGQVK DLLAESRL RYKD YIQILSSPNFS LDQYCEQMWHREKRRQRN
KGGPKWKHMQEMKKRNRRHH RDLD ELPRAVAT
```

**Important features of the protein:****Signal peptide:**

amino acids 1-36

**N-glycosylation sites.**

amino acids 139-142, 607-610, 724-727

**Tyrosine kinase phosphorylation site.**

amino acids 571-576

**Gram-positive cocci surface proteins 'anchoring' hexapeptide.**

amino acids 32-37

## **FIGURE 177**

CCCTGACCTCCCTGAGCCACACTGAGCTGGAAGCCGAGAGGTATCCTGGAGCATGCCACCAGGGAGCAGA  
 CAACCTCCCAGGTAAAGCTGGGAGCAAGACCTGAAGCTGTTCTCAGGAGCCTGGTGTATTCCCCCACCCAC  
 CTCAGCAGTTTCAGCCAGCAGGGACTGATCAGGTGTGTCAGGACTGGAGCTGGAGCAGAAGGCCTGGCTGCCAAGA  
 GTGGCCTGGAGAAAGAGGTTCAGCGCTGACCAGCGAGCTGCCGTGACTACAAGATCCAGAACCATGGGCATC  
 GGGTGAGGTGGGGGGCACAGGTGTATGTGACCTCTTGCTCAGCAAGAAGAGCTGAGAGAGGGGATCTGG  
 AGCCATTGAGGGTGTATGGAGCTACAGAGGGAGGGAAAGGTATTTAAGGTAACAGTGTGGCACAATAGTTAA  
 GAGCACAGTTTGGAGCTAGACCGACATAGGTCATAATTCTCTGTTGCTTCTAGTTCTGTAGCCCCAGGT  
 AAGGGAGTGAECTTAACCTCTGGACTCAATTCTCATCACTAAAGTAGGGCCAATAATAGCACCCACCTCAT  
 AGGGAAAGATTAATGACATAATGTATGTG**ATG**CAACTAGCAAAGTACCCAGTCCATAGTAAGTCATGCCAACAG  
 TATTTCCACCCACCCCTGTTCTGCCCCCTCCAAACCAGGTACTGCAACAGACTGGAGCAGAGGGCAGCAGGCTT  
 CAGAGCAGGGAGGCTCCAAGCATAGAACAGAGGTTACAGGAAGTGCAGAGAGCATCCGCCGGCACAGGTGAGCC  
 AGGTGAAGGGGGCTGCCCGCTGGCCCTGCTGCAGGGGGCTGGCTTAGATGTGGAGCGCTGGCTGAAGCCAGCCA  
 TGACCCAGGCCAGGATGAGGTGGAGCAGGAGCAGCGGCTCAGTGAGGCTCGGCTGCTCCAGAGGGACCTCTCTC  
 CAACCGCTGAGGATGCTGAGCTTCTGACTTTGAGGAATGTGAGGAGACGGGAGAGCTCTTGAGGAGCCTGCC  
 CCCAAGCCCTGGCCACAGGGCCCTCCCTGCCCTGACACGTGGTATTGCTATCAGGCAGGGCGTGAGGATG  
 AGCTGACAATCACGGAGGGTGAATGGCTGGAGGTATAGAGGAGGAGATGCTGACAATGGGTCAGGCTCGGA  
 ACCAGCACGGCGAGGTAGGCTTGTCCCTGAGCGATATCTCAACTTCCCGACCTCTCCCTCCAGAGAGCAGCC  
 AAGACAGTGACAATCCCTGCGGGCAGAGGCCACAGCATTCTGACAGGCTGTACAGCTACACCGGACAGA  
 GTGCAGAGGAGCTGAGCTTCCCTGAGGGGGCACTCATCCGCTGCTGCCCGGGCCAAGATGGAGTAGATGACG  
 GCTTCTGGAGGGAGAATTGGGGGGCTGTGGGGTCTTCCCTCCCTGCTGGTGGAAAGAGCTGCTTGGCCCC  
 CAGGGCACCTGAACTCTGACCCCTGACACAGATGCTGCCGCTCCCTCTCCAGCTTCTCCCCACCTGCAC  
 CTACCTCTGTGTTGGATGGGGCCCTGCACCTGCTGCTGGGACAAAGCCCTGGACTTCCCTGGGTTCTGG  
 ACATGATGGCACCTGACTCACGGCGATGCGTCCACCCACCTCCCCCGGCTAAAGCCCCGGATCCTGCCAC  
 CAGATCCCCTCAC**TGA**AGGGCAGGGAGGCTTGACCCCCAGTGAATGCTGCTGCCCTATCTCAAGCTGTCAGA  
 CCACACCATCAATGATCCAGAGCAACACAGCAAAGCTGAATGCCCTTATTTCCACCTCACCTCCAAGGGT  
 GGAAACTTGCCCTTCCCATTCTAGAGCTGAAACCCACTCCTTTTCCCATTGTTCTATCATCTTAGGACC  
 GGAACACTACCTCTCTTCTGTATGACCTATCTAGGGTGGTGAATGCCCTGAATCTCTGGGCTGGAAACC  
 ATCCATCAAGGTCTCTAGTAGTTCTGGCCACCTCTTCCCACCCCTGGCTCCATGACCCACCCACTCTGGATG  
 CCAGGGTCACTGGGTTGGGCTGGGGAGAGGAACAGGCCCTGGGAATCAGGAGCTGGAGCCAGGATGCGAAGCAG  
 CTGTAATGGTCTGAGCGGATTATTGACAATGAATAAGGGCACGAAGGCCAGGGCAGGGCCTGGGCTCTGTG  
 CTAAGAGGGCAGGGGGCTACGGTGCTATTGCTTAGGGGCCACCACGGGAGGGGCTGCTCCAGTGCAC  
 GCTCTATCATATGGAGCGAGGTGGGGGAAGGGGGCAGGCAGCCTGTTGCAGGCAGGGAGGAGAAGAGAC  
 TGAGGGCTGTGACCTCTCTGAGGCCCAAGCCTGAGACTGTGCAACTCCAGGTGGAAAGTAGAGCTGGTCCCTC  
 AGCTGGGGGCAGTGTGTCAGTGGAGGGAGGGCTTACGCCACCCACCCCTGGCTGCCAGCTGGTAG  
 TCCATCAGCACAATGAAGGAGACTTGGAGAAGAGGAATAACACTGTTGCTTCTGTTCAAGCTGTGTCAGC  
 TTTTCCCTGGGCTCCAGGACCTTCCCTACCTCACCACCAAAGGGATTATAGCAAAGGCTAACCTGC  
 AGTTTACTCTGGGGTTCAGGGAGCCGAAAGGCTAAATAGTTAAGTAGGTGATGGGAAGATGAGATTACCTCA  
 TTAGGGCTCAGGAGACACTACCTCACATACTCCCTGCTCCCTGTTGAGAGACACCTGAGAGAAAGGGGAGGG  
 TCAACAAATGAGAGACCCAGGGTAGGTGATCAGAAGCTGGGGCCACAGAGTAGAGAGCAATAAGAGGCCAGCCAGTGC  
 AGTCCCCGGCTGTGTTCTACCTGATCAGAAGTGTGCTGGTGTGGCTGCCATTGGCTCTTGAAGTGG  
 GCACGCCCTGGCTGGGGCCCTCCCTCCGGGCTCAGTGTGGCTCTGAGAAGCTGTGGCTTCCCTCAAGTG  
 CACGAGGGGTTAGGCTGCTGCTCCCTGAGTCTCCATTCTGTACTGGGGGCTGGCTAGGACCTGGGCTGTGGCC  
 TCTCAGGGGGCAGCCTCTCCATGGCAGGCATCCCTGCTGGCTGCCCTCCCCAGACCCCTGACCACCCCTG  
 GGTCTGTCCCCCACCAGAGGCCAGCTCCGTCTGTTGGGAGGCCATCACGGTGTGTCAGTCCATAGCGCT  
 TCTCAATGTGTGTCACCCGGAACCTGGAGGGAGGGAACACTGGGTTAGGACCAACTCAGAGGCTGCTTG  
 GCCCTCCCTCTGACCAGGGACATCCTGAGTTGGCTACTTCCCTGCTGGCTAAGGTAGGGAGGCCCTCTC  
 AGATTGTGGGCACATTGTGAGCCTGACTTCTGCTGGAGCTCCAGGAGGAAAGAGCCAAGGCCACCTT  
 TTGGGATCAGGTGCTGATCAGTGGGCCCTACCTCAGCCCCCTTCCCTGGAGCAGCTGCCACCTGCCCA  
 CAGAGAACACAGTGGTCTCCCTGTCGGGGGGCGCTTTCTCTGGAGCGTCCCTGACGGACAAGTGGAG  
 GCCTCTGCTGCGCTGCAATGGATGCAAGGGGCTGCAGAGGCCAGGTGCACTGTGATGATGGAGGGGCTC  
 CGTCCCTGCAAGGCTGGAGGTGGCATCCACACTGGACAGCAGGAGGGAGGTAGGGTAACATTCCATTCC  
 TCATGTTGTTCTTACGTCTTCACTGCTCTTAAACCCAGAACGCCAATTCCCCAAGGCCATT  
 TTTCTGTTCTTATCTAATAACTCAATATTAAG

**FIGURE 178**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401
><subunit 1 of 1, 370 aa, 1 stop
><MW: 40685, pI: 4.53, NX(S/T): 0
MQLAKYQSHSKSCPTVFPPPTPVLCLPNQVLQRLEQRRQQASEREAPSIEQRLQEVRESIRRA
QVSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPTAEDAELS
DFEECEETGELFEEPAPQALATRALPCPAHVVFRYQAGREDELTITGEWLEVIEEGDAEW
VKARNQHGEVGVFVPERYLNFPDLSLPESSQDSDNPCGAEPAFLAQALYSYTGQSAEELSFP
EGALIRLLPRAQDGVDDGFWRGEFGGRGVFPSLLVEELLGPPGPPELSDPEQMLPSPSPPS
FSPPAPTSVLDGPPAPVLPGDKALDFPGFLDMMAPRLRPMRPPPPPAKAPDPGHPDPLT
```

## FIGURE 179A

CACAGGGAGACCCACAGACACATATGCACGAGAGAGACAGAGGGAGGAAGAGAGACAGAGACAAGGCACAGCGGAA  
 GAAGGCAGAGACAGGGCAGGCACAGAACGGCCCAGACAGAGTCTACAGAGGGAGGGCCAGAGAACGTCAGA  
 AGACACAGGCAGGGAGAGACAAGATCCAGGAAGGGAGGGCTCAGGAGGAGAGTTGGAGAACGCCAGACCCCTGG  
 GCACCTCTCCAAGCCCAGGGACTAAGTTTCTCCATTCTTAAACGGTCTCAGCCCTCTGAAAACCTTGCC  
 TCTGACCTTGGCAGGAGTCCAAGCCCCCAGGCTACAGAGAGGAGCTTCAAAGCTAGGGTGTGGAGGACTTGGT  
 GCCCTAGACGGCCTCAGTCCCTCCCAGTCAGTACCGTGC**ATGT**CCCAGACAGGCTCGCATCCGGAGGGG  
 CTTGGCAGGGCGTGGCTGTGGGAGGCCAACCCCTGCCCTCTGCTCCCATTTGTGCCGCTCTCTGGCTGGTGTG  
 GCTGCTTCTGCTACTGCTGCCCTCTCTGCCCTCAGGCCGGCTGGCCAGCCCCCTCCCCGGAGGAGGAGAT  
 CGTGTTCAGAGAACGCTAACGGCAGCGTCTGCCCTGGCTGGCCAGGGCTGCAAGGCTGTTGTGCCGTTGCA  
 GGCCTTGGGAGACGCTGTAAGAGCTGGAGCAGGACTCCGGTGTGCAGGTGAGGGGCTGACAGTCAGTA  
 CCTGGCCAGGCCCTGAGCTGCTGGTGGAGCAGGCCCTGGCACCTACCTGACTGGCACCATCAATGGAGATCC  
 GGAGTCGGTGGCATCTCTGCACTGGATGGGGAGGCCCTGTTAGGCGTGTACAATATCGGGGGCTGAACCTCA  
 CCTCCAGCCCCCTGGAGGGAGGCACCCCTAACACTGCTGGGGACCTGGGCTCACATCCTACCCGGAAAGAGTCC  
 TGCCAGCGGTCAAGGTCCTCATGTCAACGTCAAGGCTCCTCTTGAAGCCCCAGCCCCAGACCCGAAGAGCAA  
 GCGCTTGCCTACTGAGTAGATTGTGGAGACACTGGTGGTGGCAGATGACAAGATGGCCGATTCCACGGTGC  
 GGGCTAAAGCGCTACCTGCTAACAGTGTGGCAGCAGCAGGCCCTCAAGCACCCAAAGCATTCCGAATCC  
 TGTCAGCTGGTGGTGAECTGGCTAGTGTGATCCTGGGTCAAGCAGGAGGGGCCCAAGTGGGGCCAGTGTGC  
 CCAGACCTCGCAGCTCTGTGCCTGGCAGCGGGGCTCAACACCCCTGAGGACTCGGGCCCTGACCACTTGA  
 CACAGCCATTCTGTTACCCCTCAGGACCTGTGTGGAGTCTCCACTTGCACACGCTGGTATGGCTGATGTGG  
 CACCGTCTGTGACCCGGCTGGAGCTGCTGCAATTGTGGAGGATGATGGCTCCAGTCAGCCTCACTGCTGCTCA  
 TGAACCTGGGTATGTCCTAACATGCTCATGACAACCTCAAGGCCATGCTCATCAGTTGAATGGCCTTGAGCAC  
 CTCTCGCCATGTCATGGCCCCCTGTGATGGCTCATGTGGATCCTGGAGGCCCTGGTCCCCCTGCAGTGCCTGCTT  
 CATCACTGACTTCCCTGGACAAATGGCTATGGCACTGCTCTTAGACAAACCAAGGCTCATTGCATCTGCCTGT  
 GACTTCCCTGGCAAGGACTATGATGTCGACCGCAGTGGCAGCTGACCTTGGGGCCGACTCACGCCATTGTCC  
 ACAGCTGCCGCCCTGTGCTGCCCTCTGGTGTCTGGCACCTCAATGGCCATGCCATGTGCCAGACCAAACA  
 CTCGCCCTGGGCCATGGCACACCCCTGCCGGCACAGGCCATGGTGGTCGCTGCCACATGGACCA  
 GCTCCAGGACTTCAAAATATTCCACAGGCTGGTGGCTGGGACATGGGTGACTGCTCTGGACCTG  
 TGGGGTGGTGTCCAGTTCTCTCCGAGACTGCAACGAGGGCTGTCCCCCGGAATGGCAAGTACTGTGAGGG  
 CCGCCGTACCCGCTTCCGCTCTGCAACACTGAGGACTGCCAACTGGCTCAGGCCGACCTTCCCGGAGGAGCA  
 GTGTGTCCTACAACCACCGCACCGACCTCTCAAGAGCTCCAGGGCCATGGACTGGGTCCTCGCTACAC  
 AGGCCTGGCCCCCAGGACCAGTCAAACACTCACCTGCCAGGGCCGGGACTGGCTACTACTATGTGCTGGAGCC  
 ACGGGTGGTAGATGGACCCCTGTTCCCGGACAGCTCTCGGTCTGTGTCCAGGGCGATGCATCCATGCTGG  
 CTGTGATCGCATCATTGGCTCCAAGAAGAAGTTGACAAGTGCATGGTGTGGAGGGACGGTCTGGTGTGAG  
 CAAGCAGTCAGGCTCTCAGGAAATTCAAGGTACGGATAACAACATGTGGTCACTATCCCCGGGGGCCACCCA  
 CATTCTTGTCCGGCAGCAGGAAACCCCTGGCACCCGGAGCATCTACTTGGCCCTGAAGCTGCCAGATGGCTCCTA  
 TGCCCTCAATGGTAATACACGCTGATGCCCTCCCCACAGATGTGGTACTGCCCTGGGAGTCAGCTTGCCTA  
 CAGCGGGGCACTGAGCCTCAGAGACACTGTAGGCCATGGCACTGGCCAGCCTTGAACACTGCAAGTCCT  
 AGTGGCTGGCAACCCCAAGGACACACGCCCTCCGATACAGCTCTCGTCCCCGGCCAGCCCTCAACGCCACG  
 CCCCACTCCCCAGGACTGGCTGACCGAAGAGCACAGATTCTGGAGATCCTCGGGGGCGCCCTGGCGGGCAG  
 GAAA**TAA**ACTCACTATCCGGCTGCCCTCTGGCACCGGGCTCGGACTTAGCTGGAGAAAGAGAGAGCTT  
 CTGTTGTCGCTCATGCTAAAGACTCAGTGGGAGGGCTGTGGCGTGAAGACCTGGCCCTCTCTGCCCTAAT  
 GCGCAGGCTGGCCCTGCCCTGGTTCTGCCCTGGGAGGGCAGTGTGGTTAGTGGATGGAAGGGGCTGACAGAC  
 AGCCCTCCATCTAAACTGCCCTCTGCCCTGCCGGTCACAGGAGGGAGGGGAAGGCAGGGAGGGCTGGGCC  
 CAGTTGTATTATTTAGTATTACTTACCTTTATTAGCACCAAGGGAAAGGGACAAGGACTAGGGTCTGGGAA  
 CCTGACCCCTGACCCCTCATAGCCCTCACCCCTGGGCTAGGAATCCAGGGTGTGTGATAGGTATAAGTGGT  
 TGTGTATGCGTGTGTGTGTGAAAATGTGTGTGCTTATGTATGAGGTACAACCTGTTCTGCTTCTC  
 TTGCAATTATTTATTTGGAAAAGAAAAGTCAAGGGTAGGGTGGGCTCAGGGAGGTGAGGGATTATCTTT  
 TTTTTTTCTT  
 GCACAATCTCGGCTCACTGCATCCTCCGCTCCGGGTTCAAGTGTGATTCTCATGCCCTCAGCCTCTGAGTAGCT  
 GGATTACAGGCTCTGCCACACGCCAGCTAATTTGTTGTTGTTGGAGACAGAGACTCGCTATTGTC  
 ACCAGGGCTGGAATGATTCAGCTACTGCAACCTCGCCACCTGGGTTCCAGCAATTCTCCTGCCCTCAGCCTCC  
 CGAGTAGCTGAGATTATAGGCACCTACCACGCCGGCTAATTTGTATTAGTAGAGACAGGGTTTCACCATGT  
 CATGTTGGCCAGGCTGGCTCGAACTCCTGACCTAGGTGATCCACTGCCCTCATCTCCAAAGTGTGGGATT  
 ACAGGGCTGAGGCCACCGTGCTGGCACGCCAACTAATTTGTATTAGTAGAGACAGGGTTTCACCATGT  
 TGGCCAGGCTGCTTGAACCTGACCTCAGGTAAATCGACCTGCCCTGCCCTCCAAAGTGTGGGATTACAGG  
 TGTGAGGCCACCCGGTACATATTTAAATTGAATTCTACTATTATGTGATCCTTGGAGTCAGACAG

**FIGURE 179B**

ATGTGGTTGCATCCTAACTCCATGTCTCTGAGCATTAGATTCTCATTTGCCAATAATAACCTCCCTAGAAG  
TTTGTGAGGATTAATAATGTAATAAGAACTAGCATAACACTCAAAAAAAAAAAAAAAAAGGAAA  
AAAAAAAAAAAAAAAAGGAAA

**FIGURE 180**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492
><subunit 1 of 1, 837 aa, 1 stop
><MW: 90167, pI: 8.39, NX(S/T): 1
MSQTGSHPGRGLAGRWLWGAQPCLLLPIVPLSWLVWLLLLLASLLPSARLASPLPREEEIV
FPEKLNGSVLPGSGAPARLLCRLQAFGETLLELEQDSGVQVEGLTVQYLGQAPELLGGAEP
GTYLTTGTINGDPESVASLHWGGALLGVLQYRGAEHLHQPLEGGTPNSAGGPGAHILRRKSP
ASGQGPMCNVKAPLGSPSPRPRRAKRFAASLSRFVETLVVADDKMAAFHGAGLKRYLLTVMAA
AAKAKFKHPSIRNPVSLVVTRLVILGSGEEGPVQGPSAAQTLSFCAWQRGLNTPEDSGPDHF
DTAILFTRQDLCGVSTCDTLMADVGTVCDPARSCAIVEDDGLQSAFTAHELGHVFNMHLHD
NSKPCISLNGPLSTSRRHMAPVMAHVDPPEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHL
PVTFPGKDYDADRQCQLTFGPDSRHCPCQLPPPACAALWCSGHLNGHAMCQTKHSPWADGTPCG
PAQACMGGRCLHMDQLQDFNIPQAGGWGPWGPGDCSRTCGGGVQFSSRDCTRVPVRNGGKY
CEGRRTRFRSCNTEDCPTGSALTFREEQCAAYNHRTDLFKSFPGPMWDWPRTGVAPQDQCK
LTCQARALGYYYVLEPRVVDGTPCSPDSSSVCVQGRCIHAGCDRIIGSKKFDKCMVCGGDG
SGCSKQSGSFRKFRYGYNNVTIPAGATHILVRQQGNPGHRSIYLAALKLPDGSYALNGEYTL
MPSPTDVVLPGAVSLRYSGATAASETLSGHGLAQLTLQVLVAGNPQDTRLRYSFFVPRPT
PSTPRPTPQDWLHRRAQILEILRRRPWAGRK
```

**Important features of the protein:****Signal peptide:**

amino acids 1-48

**N-glycosylation site.**

amino acids 68-71

**Glycosaminoglycan attachment site**

amino acids 188-191, 772-775

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 182-185

**Tyrosine kinase phosphorylation site.**

amino acids 730-736

**N-myristoylation sites.**

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-582, 679-684, 682-687, 763-768

**Amidation sites.**

amino acids 560-563, 834-837

**Leucine zipper pattern.**

amino acids 17-38, 24-45

**Neutral zinc metallopeptidases, zinc-binding region signature.**

amino acids 358-367

## **FIGURE 181**

CAGCAGTGGCTCTCAGCCTCTAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGG  
 CAAAGAACCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAACGCTTTAAATCC  
 AAGAAAATATGTAAATCACTTAAGATTGTGGACTGGTGTGGTATCCTGCCCTAACTCT  
 ATTGTCTGTTGGGGAGCAAGCACCTCTGCCGGAGGTACCCAAAAAGCCTATGACA  
 TGGAGCACACTTCTACAGCAATGGAGAGAAGAAGAAGATTACATGGAAATTGATCCTGTG  
 ACCAGAACTGAAATATTCAAGCGAAATGGCACTGATGAAACATTGAAAGTGCACGACTT  
 TAAAAACGGATACACTGGCATCTACTCGTGGTCTTCAAAAATGTTTATCAAAACTCAGA  
 TTAAAGTGATTCTGAATTCTGAACCAGAACAGGAAATAGATGAGAACATTAC  
 ACAACTTCTTGAACAGTCAGTGATTGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGA  
 TTTCTTAAAAATTCCAAAATTCTGGAGATTGATAACGTGACCATGTATTGGATCAATC  
 CCACTCTAATATCAGTTCTGAGTTACAAGACTTGAGGAGGGAGAACATCTCACTTT  
 CCTGCCAACGAAAAAAAGGGATTGAACAAAATGAACAGTGGTGGCCCTCAAGTGAAAGT  
 AGAGAACCGTCACGCCAGACAAGCAAGTGAGGAAGAACCTCCAATAATGACTATACTG  
 AAAATGGAATAGAATTGATCCATGCTGGATGAGAGAGGTTATTGTTGTATTACTGCCGT  
 CGAGGCAACCGCTATTGCCGCCGTCTGTGAACCTTACTAGGCTACTACCCATATCCATA  
 CTGCTACCAAGGAGGACGACTCATCTGCGTGTACATGCCCTGTAAGTGGTGGGTGGCCC  
 GCATGCTGGGAGGGCTTAAAGGAGGTTGAGCTAAATGCTAAACTGCTGGCAACATAT  
 AATAATGCATGCTATTCAATGAATTCTGCCTATGAGGCATCTGCCCTGGTAGCCAGCT  
 CTCCAGAATTACTGTAGGTAATTCTCTTCATGTTCTAAACTTACATTATCACC  
 AAAAAAAAAAAAAAAA

## **FIGURE 182**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727
><subunit 1 of 1, 317 aa, 1 stop
><MW: 37130, pI: 5.18, NX(S/T): 3
MAKNPPENCEDCHILNAEAFSKKICKSLKICGLVFGILALTLIVLFWGSKHFPEVPKKAY
DMEHTFYSGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKT
QIKVIPEFSEPEEEIDENEETTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDNVTMYWI
NPTLISVSELQDFEEEGLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDY
TENGIEFDPMELDERGYCCIYCRRGNRYCRRVCEPLLGYYPYCYQGGRVICRVIMPCNWWV
ARMLGRV
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-40

**Transmembrane domain:**

amino acids 25-47 (type II)

**N-glycosylation sites.**

amino acids 94-97, 180-183

**Glycosaminoglycan attachment sites.**

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

**N-myristoylation sites.**

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

**Microbodies C-terminal targeting signal.**

amino acids 315-317

**Cytochrome c family heme-binding site signature.**

amino acids 9-14

**FIGURE 183**

GCGGAACCTGGCTCCGGCTGGCACCTGAGGAGCGCGTGACCCCGAGGGCCCAGGGAGCTGCC  
 CGGCTGGCCTAGGCAGGCAGCCGACCATGGCCAGCACGGCGTGCAGCTCTGGGCTTCCT  
 GCTCAGCTCCTGGGCATGGTGGGCACGTTGATCACCAACCATCCTGCCGCACTGGCGGAGGA  
 CAGCGCACGTGGGCACCAACATCCTCACGGCGTGTCTACCTGAAAGGGCTCTGGATGGAG  
 TGTGTGTGGCACAGCACAGGCATCTACCAAGTGCAGATCTACCGATCCCTGCTGGCGCTGCC  
 CCAAGACCTCCAGGCTGCCCGGCCCTCATGGTCATCTCCTGCCCTCGCTCGGGCATAGCCT  
 GCGCCTGCGCCGTACGGGATGAAGTGCACGCGCTGCCAAGGGCACACCCGCCAACGACC  
 ACCTTGCCATCCTCGCGGCACCCCTTTCATCCTGGCGCCTCCTGTGCATGGTGGCGT  
 CTCCTGGACCACCAACGACGTGGTCAGAACTTCTACAACCCGCTGCTGCCAGCGGCATGA  
 AGTTTGAGATTGGCCAGGCCCTGTACCTGGCTTCATCTCCTCGTCCCTCGCTCATGGT  
 GGCACCCCTGCTTGCCTGTCCCTGCCAGGACGAGGCACCCCTACAGGCCCTACCAGGCCCGCC  
 CAGGGCCACCACGACCACTGCAAACACCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAG  
 ACAATCGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTG  
**TGA**GTCCCCACAGCCTGCTCTCCCTGGCTGCTGTGGCTGGTCCCCGGCGGGACTGTC  
 AATGGAGGCAGGGGTTCCAGCACAAAGTTACTCTGGCAATTTGTATCCAAGGAAATA  
 ATGTGAATGCGAGGAAATGTCTTAGAGCACAGGGACAGAGGGGAAATAAGAGGAGGAGAA  
 AGCTCTCTATACCAAAGACTGAAAAAAAATCCTGTCTGTTTGATTTATTATATATAT  
 TTATGTGGGTGATTGATAACAAGTTAATATAAAGTGAATTGGAGTTGGTCAGTGGGGT  
 TGGTTGTGATCCAGGAATAAACCTTGCAGGATGTGGCTGTTATGAAAAAAA

## **FIGURE 184**

MASTAVQLLGFLLSFLGMVGTLITTIPLPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIY  
QCQIYRSLLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAKGTPAKTTFAILGGTL  
FILAGLLCMVAWSWTNDVVQNPFYNPLLPSGMKFEIGQALYLGFISSSLSLIGGTLLCLSCQ  
DEAPYR PYQAPPRATTANTAPAYQPPAAYKDNRAPSVTSA THSGYRLNDYV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domains:**

amino acids 82-103, 115-141, 160-182

## **FIGURE 185**

GAGCTCCCTCAGGAGCGCGTTAGCTCACACCTCGGCAGCAGGAGGGCGGCAGCTCTCG  
 CAGGCCAGGGCGGGCGGCCAGGATCA**TG**TCCACCACATGCCAAGTGGTGGCGTTCCT  
 CCTGTCCATCCTGGGCTGGCGGCTGCATCGCGCCACCAGGATGGACATGTGGAGCACCC  
 AGGACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGC  
 GTGAGGCAGAGTTCAGGCTTACCGAATGCAGGCCATTTCACCATCCTGGACTTCCAGC  
 CATGCTGCAGGCAGTGCAGGCCGTGATGATCGTAGGCATCGCCTGGTGCCATTGGCCTCC  
 TGGTATCCATCTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCC  
 AACATGACACTGACCTCCGGATCATGTTCATGTCATTGTCTCAGGTCTTGTCAATTGCTGGAGT  
 GTCTGTGTTGCCAACATGCTGGTGAACACTTCTGGATGTCCACAGCTAACATGTACACCG  
 GCATGGGTGGGATGGTGCAGACTGTTCAGACCAGGTACACATTGGTGCAGGCTCTGGTGTG  
 GGCTGGGTGCGTGGAGGCCTCACACTAATTGGGGGTGTGATGATGTGCATGCCCTGCCGGGG  
 CCTGGCACCAGAAGAAACCAACTACAAAGCCGTTCTTATCATGCCCTCAGGCCACAGTGTG  
 CCTACAAGCCTGGAGGCTCAAGGCCAGCACTGGCTTGGGTCCAACACCAAAAACAAGAAG  
 ATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTATCCTCCAAGCACGACTA  
 TGTG**TAAT**GCTCTAACAGACCTCTCAGCACGGCGGAAGAAACTCCCAGAGCTCACCAAAA  
 AACAAAGGAGATCCCATCTAGATTCTTCTTGCTTTGACTCACAGCTGGAAAGTTAGAAAAGC  
 CTCGATTCATCTTGAGAGGCCAAATGGTCTTAGCCTCAGTCTGTCTCAAATATTCC  
 ACCATAAAACAGCTGAGTTATTATGAATTAGAGGCTATAGCTCACATTTCATCCTCTAT  
 TTCTTTTTAAATATAACTTCTACTCTGATGAGAGAATGTGGTTTAATCTCTCTCAC  
 ATTTGATGATTAGACAGACTCCCCCTTCCCTAGTCAATAAACCCATTGATGATCTA  
 TTTCCAGCTATCCCCAAGAAAACCTTGAAAGGAAAGAGTAGACCCAAAGATGTTTT  
 CTGCTGTTGAATTGTCTCCCCACCCCCAACTGGCTAGTAATAAACACTTACTGAAGAA  
 GAAGCAATAAGAGAAAGATATTGTAATCTCTCCAGCCATGATCTGGTTTCTTACACTG  
 TGATCTAAAAGTTACCAAACAAAGTCATTTCAGTTGAGGCAACCAAACCTTCTACTG  
 CTGTTGACATCTCTTATTACAGCAACACCATTCTAGGAGTTCTGAGCTCTCCACTGGAG  
 TCCTCTTCTGCGGGTCAGAAATTGCCCTAGATGAATGAGAAAATTATTTTTAAT  
 TTAAGTCCTAAATATAGTTAAAATAATGTTAGTAAATGATACTATCTCTGTGA  
 AATAGCCTCACCCCTACATGTGGATAGAAGGAAATGAAAAATAATTGCTTGACATTGTCT  
 ATATGGTACTTGTAAAGTCATGCTTAAGTACAATTCCATGAAAAGCTCACACCTGTAATC  
 CTAGCACTTGGGAGGCTGAGGAGGAAGGATCACCTGAGGCCAGAAGTCTGAGGACTAGCCTG  
 GGCAACATGGAGAAGCCCTGTCTCACAAATACAGAGAGAAAAATCAGCCAGTCATGGTG  
 GCATACACCTGTAGTCCCAGCATTCCGGAGGCTGAGGTGGGAGGATCACTTGAGGCCAGGG  
 AGGTTGGGCTGCAGTGAGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCGAGA  
 TCCTGTCTAAAAAATAAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAAA  
 ACTAATTCTTAA

## **FIGURE 186**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734
><subunit 1 of 1, 261 aa, 1 stop
><MW: 27856, pI: 8.50, NX(S/T): 1
MSTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLWRSCVRQSSGFT
CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIM
FIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTL
IGGVMMCIACRGLAPEETNYKAVSYHASGHHSVAYKPGGFCASTGFGSNTKNKKIYDGGARTE
DEVQSYP SKHDYV
```

**Signal peptide:**

amino acids 1-23

**Transmembrane domains:**

amino acids 81-100, 121-141, 173-194

## **FIGURE 187**

GGAAAAACTGTTCTCTGTGGCACAGAGAACCCCTGCTCAAAGCAGAAGTAGCAGTTCCG  
 GAGTCCAGCTGGCTAAAACATCCCAGAGGATA**ATG**GCAACCCATGCCTAGAAATCGCTG  
 GGCTGTTCTGGTGGTGGAAATGGTGGGCACAGTGGCTGCACTGTCATGCCTCAGTGG  
 AGAGTGTGCGGCCTTCATTGAAAACAACATCGTGGTTTGAAAACCTCTGGGAAGGACTGTG  
 GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGG  
 CTCTTCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGCTGCTCCGTGATGTCCTTC  
 TTGGCTTCATGATGCCATCCTGGCATGAAATGCACCAGGTGCACGGGGACAATGAGAA  
 GGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTCATCACGGGCATGGTGGTGC  
 TCATCCCTGTGAGCTGGGTTGCCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAAT  
 GTGCCCAAAACGTGAGCTGGAGAACGCTCTACTTAGGATGGACACGGCACTGGTGCT  
 GATTGTTGGAGGAGCTGTTCTGCTGCGTTTTGTTGCAACGAAAAGAGCAGTAGCTACA  
 GATACTCGATACTTCCCATCGCACAAACCAAAAAAGTTATCACACCGAAAGAAGTCACCG  
 AGCGTCTACTCCAGAAGTCAGTATGTG**TAG**TTGTGTATGTTTTAACTTTACTATAAGC  
 CATGCAAATGACAAAATCTATATTACTTTCTCAAATGGACCCAAAGAAACTTGATTAA  
 CTGTTCTTAACTGCCTAATCTAATTACAGGAACGTGCACTCAGCTATTATGATTCTATAA  
 GCTATTCAGCAGAATGAGATATTAAACCAATGCTTGATTGTTCTAGAAAGTATAGTAAT  
 TTGTTCTAAGGTGGTCAAGCATCTACTCTTTATCATTACTCAAATGACATTGCT  
 AAAGACTGCATTATTTACTACTGTAATTCTCACGACATAGCATTATGTACATAGATGAG  
 TGTAACATTTATCTCACATAGAGACATGCTTATGGTTATTAAAATGAAATGCCAG  
 TCCATTACACTGAATAAATAGAACTCAACTATTGCTTTCAGGGAAATCATGGATAGGGTTG  
 AAGAAGGTTACTATTAAATTGTTAAAACAGCTAGGGATTAATGTCCTCCATTATAATGA  
 AGATTAATGAAGGCTTAATCAGCATTGTAAGGAAATTGAATGGCTTCTGATATGCTG  
 TTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTATCCTCTTCCAGAGGCTTTTT  
 TTCTTGTGTATTAATTAACATTAAACATTAAACGCACTATTGTCAGGGCTTGCATTCA  
 AACTGCTTCCAGGGCTACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAGTGTG  
 GTTTAGGAAAGTGAATTTGTTTGATTTGAAGAAGAATGATGCATTGACAA  
 GAAATCATATGTATGGATATATTAAAGTATTGAGTACAGACTTGAGGTTCATC  
 AATATAAATAAAAGAGCAGAAAAATGTCTGGTTTCATTGCTTACCAAAAAACAAACA  
 ACAAAAAAAAGTTGTCCTTGAGAACCTCACCTGCTCCTATGTGGGTACCTGAGTC  
 AAAATTGTCATTGTTCTGTGAAAAATAAATTCCCTTCTGTACCACTTTCTGTTAGTT  
 ATCTGTAAATACTGTATTTCTGTTATTCAAATTGATGAAACTGACAATCCAATTGA  
 AAGTTGTCGACGTCTGTCTAGCTTAAATGAATGTGTTCTATTGCTTATACATTATA  
 TTAATAAATTGTACATTCTAATT

## **FIGURE 188**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735
><subunit 1 of 1, 225 aa, 1 stop
><MW: 24845, pI: 9.07, NX(S/T): 0
MATHALEIAGLFLGGVGMVGTAVTVMPQWRVSAFIENNIVVFENFWEGLWMNCVRQANIRM
QCKIYDSLLALSPDLQAARGLMCAASVMSFLAFMAILGMKCTRCTGDNEKVKAHILLAGI
IFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVF
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV
```

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 82-101, 118-145, 164-188

## **FIGURE 189**

TCGCC**ATG**GCCTCTGCCGGAATGCAGATCCTGGGAGTCGTCCGTACACTGCTGGCTGGTG  
 AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTCATCGGCAACAGCAT  
 CGTGGTGGCCCAGGTGGTGTGGGAGGGCCTGTGGATGTCCTGCGTGGTGCAGAGCACCGGCC  
 AGATGCAGTGCAAGGTGTACGACTCACTGCTGGCGCTGCCACAGGACCTGCAGGCTGCACGT  
 GCCCTCTGTGTCATGCCCTCCTGTGGCCCTGTTGGCTGCTGGTCTACCTGCTGGGC  
 CAAGTGTACCACCTGTGTGGAGGAGAAGGATTCCAAGGCCGCTGGTGCACCTCTGGGA  
 TTGTCTTGTCATCTCAGGGTCTGACGCTAATCCCCGTGTGCTGGACGGCGATGCCATC  
 ATCCGGGACTTCTATAACCCCCCTGGTGGCTGAGGCCAAAAGCGGGAGCTGGGGGCCTCCCT  
 CTACTTGGGCTGGCGGCCTCAGGCCCTTTGTTGCTGGTGGGGGTTGCTGTGCTGCACTT  
 GCCCCTCGGGGGGTCCCAGGGCCCCAGCCATTACATGGCCCGCTACTCAACATCTGCCCT  
 GCCATCTCTCGGGGGCCCTCTGAGTACCCCTACCAAGAATTACGT**TGA**CGTGGAGGGAAATG  
 GGGGCTCCGCTGGCGCTAGGCCATCCAGAAGTGGCAGTGCCAACAGCTTGGATGGGTT  
 CGTACCTTTGTTCTGCCTCCTGCTATTTCTTTGACTGAGGATATTAAAATTCAATT  
 GAAAATGAGCCAAGGTGTTGACTCAGACTCTCACTTAGGCTCTGCTGTTCTCACCTTGG  
 ATGATGGAGCCAAGAGGGATGCTTGAGATTCTGGATCTTGACATGCCATCTAGAAGC  
 CAGTCAAGCTATGAACTAATGCGGAGGCTGCTGCTGGCTTGCAACAAGACAGAC  
 TGTCCTCAAGAGTTCCCTGCTGCTGGCTGGGGCTGGCTTCCCTAGATGTCAGGACAGCTG  
 CCCCCCATCCTACTCAGGTCTCTGGAGCTCCTCTTCACCCCTGGAAAAACAAATCATCTG  
 TTAACAAAGGACTGCCACCTCCGGAATTCTGACCTCTGTTCTCCGTCTGATAAGACG  
 TCCACCCCCCAGGGCCAGGTCCCAGCTATGTAGACCCCCGCCACCTCAAACACTGCACC  
 CTTCTGCCCTGCCCTCGTCTCACCCCTTACACTCACATTATCAAATAAGCATG  
 TTTGTTAGTGCA

## **FIGURE 190**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736
><subunit 1 of 1, 220 aa, 1 stop
><MW: 23292, pI: 8.43, NX(S/T): 0
MASAGMQILGVVLTLLGWVNGLVSCALPMWKVTAFIGNSIIVVAQVVWEGLWMSCVVQSTGQM
QCKVYDSLLALPQDLQAARALCVIALLVALFGLLVYLAGAKCTTCVEEKDSKARLVLTS
FVISGVTLIIPVCWTAHAIIRDFYNPLVAEAQKRELGASLYLGWAASGLLLLGGGLLC
SGGSQGPSPHYMARYSTSAPAISRGPSEYPTKNYV
```

**Transmembrane domains:**

amino acids 8-30 (type II), 82-102, 121-140, 166-186

**FIGURE 191**

GC CAAGGAGAACATCATCAAAGACTTCTAGACTCAAAAGGCTCACGTTACATCTG  
AGCATCTTCTACCACTCCGAATTGAACCAGTCTTCAAAGTAAAGGCAATGGCATTATCCC  
TTGCAAATTGCTGGCTGGTCTGGGTCCTGGCATGGTGGGACTCTGCCACAACCCT  
TCTGCCCTCAGTGGTGGAGTATCAGCTTGTTGGCAGCAACATTATTGTCTTGAGAGGGCTC  
TGGGAAGGGCTCTGGATGAATTGCATCCGACAAGCCAGGGTCCGGTTGCAATGCAAGTTCTA  
TAGCTCCTTGGCTCTCCCGCCTGCCCTGGAAACAGCCCGGGCCCTCATGTGTGGCTG  
TTGCTCTCTCCTTGATGCCCTGCTTATTGGCATCTGTGGCATGAAGCAGGTCCAGTGCACA  
GGCTCTAACGAGAGGGCAAAGCATACCTTCTGGGAACCTCAGGAGTCCTCTTCATCCTGAC  
GGGTATCTCGTTCTGATTCCGGTGAGCTGGACAGCCAATATAATCATCAGAGATTCTACA  
ACCCAGCCATCCACATAGGTAGAAACGAGAGCTGGAGCAGCACTTTCTGGCTGGCA  
AGCGCTGCTGTCCTCTCATTGGAGGGGTCTGCTTGATTTGCTGCTGCAACAGAAA  
GAAGCAAGGGTACAGATATCCAGTGCCTGGCTACCGTGTGCCACACACAGATAAGCGAAGAA  
ATACGACAATGCTTAGTAAGACCTCCACCAAGTTATGTCTAATGCCTCCTTGGCTCCAAGT  
ATGGACTATGGTCAATGTTTTATAAAGTCCTGCTAGAAACTGTAAGTATGTGAGGCAGGA  
GAACCTGTTATGTCTAGATTACATTGATACGAAAGTTCAATTGTTACTGGTGGTAGG  
AATGAAAATGACTTACTTGGACATTCTGACTTCAGGTGTATTAAATGCATTGACTATTGTTG  
GACCCAATCGCTGCTCCAATTTCATATTCTAAATTCAAGTATAACCCATAATCATTAGCAAG  
TGTACAATGATGGACTACTTATTACTTTGACCACATGTATTATCTGATAAGAATCTAAA  
GTTGAAATTGATATTCTATAACAATAAAACATACCTATTCTA

## **FIGURE 192**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737
><subunit 1 of 1, 173 aa, 1 stop
><MW: 18938, pI: 9.99, NX(S/T): 1
MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLIGICGMKQVQCTGSNER
AKAYLLGTSGVLFILTGIFVLI PVSWTANIIIRD FYNPAIHIGQKRELGAALFLGWASAAVL
FIGGGLLCGFCCCNRKKQGYRYPVPGYRPHTDKRRNTTMLSKTSTSYY
```

**Important features of the protein:**

**Transmembrane domains:**

amino acids 31-51, 71-90, 112-133

**N-glycosylation site.**

amino acids 161-164

**FIGURE 193**

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTCCAGC**ATG**AAGATCACTGGGGT  
CTCCTTCTGCTCTGTACAGTGGTCTATTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCC  
AAAAAAAGTGGACTGCAGCATTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCATCA  
CATACCTACCAGTTGTGGTTCTGACTACATCACCTATGGGAATGAATGTCATTGTGTACC  
GAGAGCTTGAAAAGTAATGGAAGAGTTCAGTTCTCACGATGGAAGTTGC**TAA**ATTCTCCA  
TGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTCATCCCAGGCTCTGACTG  
AGTTTCTTCAGTTTACTGATGTTCTGGGTGGGGACAGAGCCAGATTGAGTAATCTG  
ACTGAATGGAGAAAGTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCAT  
TTTTTTTTAACACGTCAATAAAAAATAATCTCCCAGA

## **FIGURE 194**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73739
><subunit 1 of 1, 85 aa, 1 stop
><MW: 9232, pI: 7.94, NX(S/T): 0
MKITGGLLLLCTVVYFCSSSEAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGN
ECHLCTESLKSNGRVQFLHDGSC
```

**Signal peptide:**

amino acids 1-19

**FIGURE 195**

CCCGCGCCC GGTTCTCCCTCGCAGCACCTCGAAGTGC GCCCTCGCCCTCCTGCTCGCGCCC  
CGCCGCCATGGCCTGCCCTCCCCCGCGGCCCTGCTGTCCCTGCCCTGACCGGGCTGGCGCTGC  
TCCTGCTCCTGTGCTGGGCCAGGTGGCATAAGTGGAAATAAACTCAAGCTGATGCTCAA  
AAACGAGAACGACCTGTTCCA ACTAAGACTAAAGTGGCCGTTGATGAGAATAAAGCAAAGA  
ATTCCCTGGCAGCCTGAAGCGCCAGAACGGCAGCTGTGGGACCGGACTCGGCCGAGGTGC  
AGCAGTGGTACCAGCAGTTCTACATGGCTTGATGAAGCGAAATTGAAGATGACATC  
ACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCA  
CTATGATGAAGACTCTGCAATTGGTCCCCGGAGCCCTACGGCTTAGGCATGGAGCCAGCG  
TCAACTACGATGACTTAACCATGACTGCCACACGCTGTACAAGAACAAATAGCGATT  
TCTTCATGTATCTCCTAATGCCCTACACTACTTGGTTCTGATTTGCTCTATTCAAGCAGAT  
CTTTTCTACCTACTTGTGATCAAAAAAGAAGAGTTAAAACAACACATGAAATGCCTT  
TGATATTCATGGGAATGCCTCTCATTTAAAAATAGAAATAAAGCATTGTTAAAAGA

## **FIGURE 196**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742
><subunit 1 of 1, 148 aa, 1 stop
><MW: 17183, pI: 8.77, NX(S/T): 0
MAASPARPAVLALTGLALLLLCWGP GGISGNKLKLMQKREAPVPTKTKAVDENAKEFL
GSLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRNGHEY YGDYYQRHYD
EDSAIGPRSPYGFRHGASVNYDDY
```

**Signal peptide:**

amino acids 1-30

**FIGURE 197**

CGGCTCGAGCCGCCCGGAAGTCCCCGAGGGGCCGATGGAGCTGGGGAGCCGGCGCTC  
 GGTAGCGCGGGCAAGGCAGGC**TG**ACCCCTGATTGAAGGGTGGGTATGAGGTGAC  
 CGTCCTTTCTCGGTGCTTGCTGCCTCTGGTGCAGGCCCTGCCTGGTCTAACGCACA  
 CCGCTGAGGGCGGGGACCCACTGCCAGCCGTAGGGACCCAAACGCCATCCCAGCCCAGC  
 GCAGCCATGGCAGCTACCGACAGCATGAGAGGGAGGCCAGGGCAGAGACCCCCAGCCT  
 GAGACACAGAGGTCAAGCTGCACAGCCAGAGCCAGCACGGGTTACAGCAACACGCCAG  
 CCCCGGACTCCCCGAGGAGCCCTCGTGCACGGCTGAAATTCTCAATGATTAGCAGAGCAG  
 GTGGCCAGGGCTGGCCCCACGACACCATTGGCTCTGAAAAGGACCCAGTTCCGGCCG  
 GGAACAGCAGGTGCGACTCATCTACCAAGGGCAGCTGCTAGGCGACGACACCCAGACCCCTGG  
 GCAGCCTTCACCTCCCTCCAACTCGTTCTCCACTGCCACGTGTCCACGAGAGTCGGTCCC  
 CCAAATCCCCCTGCCGCCGGGTCCGAGCCGCCCTCCGGGCTGGAAATCGGCAGCCT  
 GCTGCTGCCCTGCTGCTCTGCTGTTGCTGCTCTGGTACTGCCAGATCCAGTACCGGC  
 CCTTCTTCCCCGTACCGCCACTCTGGCCTGGCCGGCTCACCTGCTCAGTCTCCTG  
 GCCTTGCCATGTACCGCCCG**TAGT**GCCTCCGCCGGCGCTTGGCAGCGTCGCCGGCCCTCC  
 GGACCTTGCTCCCCGCCGCCGGAGCTGCTGCCTGCCAGGCCGCCCTCCGGCCTG  
 CCTCTCCCGCTGCCCTGGAGCCAGCCCTGCCAGAGGACTCCGGGACTGGCGGAGG  
 CCCCGCCCTGCGACCGCCGGGCTGGGCCACCTCCCGGGCTGCTGAACCTCAGCCCGCA  
 CTGGGAGTGGGCTCTCGGGCATCTGCTGCTGCTGCCCTGCCGGCAGAGCCG  
 GGCGCCCCGGGGCCGTCTTAGTGTGCTGCCGGAGGACCCAGCCGCCTCCAATCCCTGAC  
 AGCTCCTGGCTGAGTTGGGACGCCAGGTGGTGGAGGCTGGTAAGGGAGCGGGAG  
 GGGCAGAGGAGTTCCCCGAAACCGTGCAGATTAAAGTAAGTGAAGTTAAAAAAA  
 AAAAAAAA

## **FIGURE 198**

MTLIEVGDEVTVLFSVLACLLVLALAWVSTHTAEGGDPLPQPSGTPPSQPSAAMAATDSM  
RGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVRLKFLNDSEQVARAWPHDT  
IGSLKRTQFPGREQQVRЛИYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRVGPPNPPCPPGS  
EPGPSGLEIGSLLLPLLWYCQIQYRPFFPLTATLGLAGFTLLSLLAFAMYRP

**Signal peptide:**

amino acids 1-31

**Transmembrane domain:**

amino acids 195-217

**FIGURE 199**

GAGATTGGAAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCCAG  
ATTCCCCAGGCTCTCAGAGAAGATCAGCAGAAAGTCTGCAAGACCCTAACGAACCATCAGCCC  
TCAGCTGCACCTCCTCCCTCCAAGG**ATG**ACAAAGGCGCTACTCATCTATTGGTCAGCAGC  
TTTCTTGCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTGGCCCAAGGTGCTGCAGCT  
GGAGGACTTGGATGGGTTGAGGGTTACTCCCTGAGTGACTGGCTGTGCCTGGCTTTGTGG  
AAAGCAAGTTCAACATATCAAAGATAAAATGAAAATGCGGATGGAAGCTTGACTATGGCCTC  
TTCCAGATCAACAGCCACTACTGGTGCAACGATTATAAGAGTTACTCGAAAAACCTTGCCA  
CGTAGACTGTCAAGATCTGCTGAATCCAACCTTCTGCAGGCATCCACTGCGAAAAAGGA  
TTGTGTCCGGAGCACGGGGATGAACAACTGGGTAGAATGGAGGTTGCACTGTTCAGGCCGG  
CCACTCTCCTACTGGCTGACAGGATGCCGCTGAGA**TGA**ACAGGGTGCAGGTGCACCGTGG  
AGTCATTCCAAGACTCCTGTCCACTCAGGGATTCTCATTCTTCTTCCACTGCCTCCA  
CTTCATGTTATTTCTTCCCTCCATTACAACAAACTGACCAGAGCCCCAGGAATAAA  
TGGTTTCTGGCTTCCCTTACTCCCATCTGGACCCAGTCCCTGGTCTGTCTGTTAT  
TTGTAAACTGAGGACCACAATAAAGAAATCTTATATTATCG

## **FIGURE 200**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746
><subunit 1 of 1, 148 aa, 1 stop
><MW: 16896, pI: 6.05, NX(S/T): 1
MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCLAFVESKFNISKI
NENADGSFDYGLFQINSHYWCNDYKSYSSENLCVDCQDLLNPNLLAGIHCAKRIVSGARGMN
NWVEWRLHCSGRPLSYWLTGCRLR
```

**Signal peptide:**

amino acids 1-18

## **FIGURE 201**

TCTGACCTGACTGGAAGCGTCAAAGAGGGACGGCTGTCAAGCCCTGCTTGACTGAGAACCCA  
CCAGCTCATCCCAGACACCTCATAGCAACCTATTATACAAAGGGGAAAGAAACACCTGAG  
CAGAATGGAATCATTATTTTCCAAAGGAGAAAACCGGGTAAAGGGAGGGAAAGCAATT  
AATTGAGTCCTGTGAATGGGCTTCAGAAGGCAATTAAAGAAATCCACTCAGAGAGGAC  
TTGGGTGAAACTGGGTCTGTGGTTCTGATTGTAAGTGGAAAGCAGGTCTGCACACGC  
TGTTGCCAAATGTCAGGACCAGGTTAAGTGACTGGCAGAAAAACTCCAGGTGAAACAAGCA  
ACCCATGTTCTGCTGCAAGCTGAGGAGCCTGGAGCAGGGAGAAAGCTAAGTGAACATGAC  
CTGTTGCATTGGCAAGTTCTAGCAAC**ATG**CTCTAAGGAAGCGATAACAGGCACAGACCAG  
CAGACTCCAGTCCTCCTGCTCCTGATGCTGGATGCGTCCTGATGATGGTGGCGATG  
TGCACCCCTCCCCACCACACCCCTGACAGACTGTCACAGCCCAAGCCAGCAAGCACAGCC  
GAAGCCAGGTACCGCCTGGACTTGGGAATCCAGGATTGGTACTGGAAGCTGAGGATGA  
GGGTGAAGAGTACAGCCCTCTGGAGGGCCTGCCACCCCTTATCTACTGCGGGAGGATCAGC  
TGCTGGTGGCGTGGCCTACCCCAGGCCAGAAGGAACCAGAGCCAGGGCAGGAGAGGTGG  
AGCTACCGCCTCATCAAGCAGCCAAGGAGCAGGATAAGGAAGCCCCAAAGAGGGACTGGGG  
GGCTGATGAGGACGGGGAGGTGCTGAAGAAGAGGAGTTGACCCGTTAGCCTGGACCCAC  
GTGGCCTCCAGGAGGCACTCAGTGCCGCATCCCCCTCCAGAGGGCTGCCCCAGGAGTGG  
CACCCACTGTGTCAGCAGCACCCCTCAGGACAGCCTGCCACAGCCAGCGTCATCCTCTG  
TTTCATGATGAGGACGGCTGGTCCACTCTCCTGCGGACTGTACACAGCATTGACACAGTGC  
CCAGGGCCTCCTGAAGGAGATCATCCTCGTGGACGACCTCAGCCAGCAAGGACAACCTCAAG  
TCTGCTCTAGCGAATATGTGGCCAGGCTGGAGGGGGTGAAGTTACTCAGGAGCAACAAGAG  
GCTGGGTGCCATCAGGGCCCGGATGCTGGGGGCCACCAGAGCCACCAGGGATGTGCTGCT  
TCATGGATGCCACTGCCAGTGCCACCCAGGCTGGCTGGAGGCCCTCCTCAGCAGAATAGCT  
GGTGACAGGAGGCCAGTGGTATCTCCGGTGTAGATGATGTTGACTGGAAGACTTCCAGTA  
TTACCCCTCAAAGGACCTGCAGCGTGGGGTGTGGACTGGAAGCTGGATTCCACTGGAAC  
CTTGCCAGAGCATGTGAGGAAGGCCCTCCAGTCCCCATAAGCCCCATCAGGAGCCCTGTG  
GTGCCCGAGAGGTGGTGGCCATGGACAGACATTACTCCAAAACACTGGAGCGTATGACTC  
TCTTATGTCGCTGCAGGGTGGTAAAACCTCGAACTGTCTTCAAGGCCTGGCTCTGTTG  
GCTCTGTTGAAATCCTCCCTGCTCTCGGGTAGGACACATCTACAAAATCAGGATTCCCAT  
TCCCCCTGACCAGGAGGCCACCTGAGGAACAGGGTTCGATTGCTGAGACCTGGCTGG  
GTCATTCAAAGAAACCTCTACAAGCATAGCCCAGAGGCCCTCTCCTGAGCAAGGCTGAGA  
AGCCAGACTGCATGGAACGCTTGCAGCTGCAAAGGAGACTGGGTTGTCGGACATTCCACTGG  
TTTCTGGCTAATGTCTACCCCTGAGCTGTACCCATCTGAACCCAGGCCAGTTCTCTGGAAA  
GCTCCACAACACTGGACTTGGCTCTGTGCAGACTGCCAGGAGCAAGGGGACATCCTGGCT  
GTCCCAGGGTGTGGCTCTTGCAGTGACAGCCGGAGCAACAGTACCTGCAGCACACCAGC  
AGGAAGGAGATTCACTTGGCAGGCCACAGCACCTGTGCTTGCTGTCAGGAGGAGCAGGT  
GATTCTTCAGAACTGCACGGAGGAAGGCCATCCACCGCAGCACTGGGACTTCCAGG  
AGAATGGGATGATTGTCACATTCTTCTGGAAATGCATGGAAGCTGTGGTGCAGGAA  
AATAAGATTGTACCTGCGTCCGTGTGATGGAAAAGCCGCCAGCAGTGGCAGTGG  
GATAAAATGCTGTGGATGAACGA**TGA**ATGTCAATGTCAGAAGGAAAAGAGAAATT  
AAAATCCAGCTCAAGTGAACGTAAGAGCTTATATATTTCATGAAGCTGATCCTTTGTG  
GTGTGCTCTTGTGTTAGGAGAGAAAAAGCTCTATGAAAGAATATAGGAAGTTCTCCTT  
TCACACCTTATTTCATTGACTGCTGGCTGCTTA

**FIGURE 202**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760
><subunit 1 of 1, 639 aa, 1 stop
><MW: 73063, pI: 6.84, NX(S/T): 2
MLLRKRYRHRPCRLQFLLLLLMLGCVLMVVAMLHPPHHTLHQTVTAQASKHSPEARYRLDFG
ESQDWVLEAEDEGEYEYSPLEGPPFISLREDQLLVAVALPQARRNQSQGRGGSYRLIKQPR
RQDKEAPKRDWGADEDGEVSEEEELTPFSLDPRLQEAALSARIPLQRALPEVRHPLCLQQHP
QDSLPTASVILCFHDEAWSTLLRTVHSILDTPRAFLKEIILVDDLSQQGQLKSALSEYVAR
LEGVKLLRSNKRLGAIRARMLGATRATGDVLVFMDAHCECHPGWLEPLLSRIAGDRSRVVSP
VIDVIDWKTQYYPSKDLQRGVLDWKLDFHWEPLPEHVRKALQSPISPIRSPVVPGEVVAMD
RHYFQNTGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGHIYQNQDSHSPLDQEATL
RNRVRIAETWLGSFKETFYKHSPEAFSLSKAEKPDCMERLQLQRRLGCRTFWFLANVYPEL
YPSEPRPSFSGKLHNTGLGLCADCQAEGDILGCPVLAPCSDSRQQYLQHTSRKEIHFGSP
QHLCAVRQEQQVILQNCTEEGLAIHQHQHWDFQENGIVHILSGKCMEAVVQENNKDLYLRPC
DGKARQQWRFDQINAVDER
```

**Signal peptide:**

amino acids 1-28

## **FIGURE 203**

CGCCAAGCATGCAGTAAAGGCTGAAAATCTGGGTACAGCTGAGGAAGACCTCAGAC**ATGGA**  
 GTCCAGGATGTGGCCTGCGCTGCTGCTGCCAACCTCCCTCTGGCCACTGCTGTTGC  
 TGCCCCCTCCCACCGCCTGCTCAGGGCTCTCATCCTCCCCCTGAACCCCACCAGCCCCAGCC  
 CGCCCCCCCCTGTGCCAGGGGAGGCCCTCGGCCCCACGTATGTGTGCGTGTGGGAGCGAGC  
 ACCTCCACCAAGCCGATCTCCTCGGGTCCAAGATCACGTCGGCAAGTCCTGCCTGGCACTG  
 CACCCCCAGCCACCCATCAGGCTTGAGGAGGGCCGCCATCCCCAATACCCCTGGGCT  
 ATCGTGTGGGTCCCACCGTGTCTCGAGAGGATGGAGGGACCCCAACTCTGCCAATCCCGG  
 ATTTCTGGACTATGGTTTGAGGCCCTCATGGGCTCGCAACCCCACACCCCAACTCAGACT  
 CCATGCGAGGTGATGGAGATGGCTTATCCTGGAGAGGCACCTGCCACCCCTGCGGCCATT  
 CTGTTCGGGGCCGTGGGAAGGTGTGGACCCCCAGCTCTATGTCACAATTACCATCTCCAT  
 CATCATTGTTCTCGTGGCCACTGGCATCATCTTCAAGTTCTGCTGGGACCGCAGCCAGAAGC  
 GACGCAGACCCCTCAGGGCAGCAAGGTGCCCTGAGGCAGGAGGAGGCCAGCAGCCACTGACA  
 GACCTGTCCCCGGCTGGAGTCACTGTGTGGGGCTTCGGGACTCACCTACCCCCACCCC  
 TGACCATGAGGAGCCCCGAGGGGACCCGGCTGGGATGCCCAACCCCAAGGGGCTCCAG  
 CCTTCCAGTTGAACCGG**TGA**GGGCAGGGCAATGGGATGGGAGGGCAAAGAGGGAAAGGAAAC  
 TTAGGTCTTCAGAGCTGGGTGGGGTGCCCTCTGGATGGTAGTGAGGAGGCAGGCAGGCGTGGC  
 CTCCCACAGCCCTGGCCCTCCAAGGGGCTGGACAGCTCCTCTGGGAGGCACCCCTTC  
 CTTCTCCCAGTCTCAGGATCTGTGTCTATTCTCTGCTGCCATAACTCCAACCTGCCC  
 TCTTGGTTTTCTCATGCCACCTGTCTAAGACAACCTGCCCTTTAACCTTGATTCCC  
 CCTCTTGTCTGAACCTCCCTCTATTCTGGCTACCCCTGGTTCTGACTGTGCCCTT  
 TCCCTCTCCTCTCAGGATTCCCTGGTAATCTGTGATGCCCAATGTTGGGTGCAGCC  
 AAGCAGGAGGCCAAGGGGCCGGCACAGCCCCCATCCACTGAGGGTGGGGCAGCTGTGGGA  
 GCTGGGCCACAGGGCTCTGGCTCTGCCCTTGACACACCACCCGAACACTCCCCAGCC  
 CCACGGCAATCCTATCTGCTGCCCTCTGCAGGTGGGGCCTCACATATCTGTGACTTCG  
 GGTCCCTGTCCCCACCCCTGTGCACTCACATGAAAGCCTGACACTCACCTCCACCTTCAC  
 AGGCCATTGACACGCTCCTGCACCCCTCTCCCGTCCATACCGCTCGCTAGCTGACTCT  
 CATGTTCTCTCGTCTCACATTTGCACTCTCCTTCCCACATTCTGTGCTAGCTCACAG  
 TGGTCAGCGTTCTGCACACTTACCTCTCATGTGCGTTCCCGGCCATGTTGTGGTGG  
 TGTGCGCGTGTGTCACTCTCTCCCTCATGAACACCCACCCACCTCGTTCCGCAGCCCTGC  
 GTGCTGCTCCAGAGGTGGGTGGGAGGTGAGCTGGGGCTCTGGGCCATCGGTATGG  
 TCTCGCCATCCACACCATTGTTCTGTCTCCCCATCCTACTCCAAGGATGCCGGCA  
 TCACCCCTGAGGGCTCCCCCTGGGAATGGGGTAGTGAGGCCAGACTTCACCCCCAGCCCA  
 CTGCTAAAATCTGTTCTGACAGATGGGTTTGGGGAGTCGCCTGTCAGTACATGAGAA  
 AGGGACTCCCATTGCCCTCCCTTCTCACAGTCCCTTGTCTGTCTGGCT  
 TCTGTGTGTGCCCCATTCTCTGGACTTCAGAGCCCCCTGAGCCAGTCTCCCTCCAGCCT  
 CCCTTGGGCCCTCCCTAACCTCACCTAGGCTGCCAGGGACCGGGAGTCAGCTGGTTCAAGGCC  
 ATCGGGAGCTGCCTCCAAGTCTACCCCTCCCTCCGGACTCCCTCCTGGCTCCCT  
 CCTCCCTCCTCCACTCTCCTTGTCTTCCACCTTCCCTCCCTTCCCTGGCTCCCTAGGCT  
 GTGATATATATTTGTATTATCTCTTCTTCTTGTGGTGTGATCATCTGAATTACTGTG  
 GGATGTAAGTTCAAAATTTCAAATAAGCCTTGCAAGATAA

## **FIGURE 204**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393
><subunit 1 of 1, 243 aa, 1 stop
><MW: 26266, pI: 8.43, NX(S/T): 1
MRPQGPAAASPQRLRGLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV
PGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRNSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGPLPIEAIYLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIIEELPK
```

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217

**FIGURE 205**

GTAAACCAGCGCAGTCCTCCGTGCGTCCGCCGCTGCCCTCACTCCCAGGATGG  
CATCCTGTCTGGCCCTGCGCATGGCGCTGCTGGTCTCCGGGTTCTGGCCCTGCGGTG  
CTCACAGACGATGTTCCACAGGAGCCGTGCCCACGCTGTGGAACGAGCCGGCGAGCTGCC  
GTCGGGAGAAGGCCCCGTGGAGAGCACCAGCCCCGGCCGGAGCCGTGGACACCGGTCCCC  
CAGCCCCCACCGTCGCCAGGACCCGAGGACAGCACCGCGCAGGAGCGGCTGGACCAGGC  
GGCGGGTCGCTGGGCCCGCGCTATCGCGGCCATCGTATCGCCGCCCTGCTGGCACCTG  
CGTGGTGCTGGCGCTCGTGGTCGCGCTGAGAAAGTTTCTGCCTCCTGAAGCGAATAAA  
GGGGCCGCGCCCGGCCGCGCGACTCGGAAAAAAAAAAAAAA

## **FIGURE 206**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398
><subunit 1 of 1, 121 aa, 1 stop
><MW: 12073, pI: 4.11, NX(S/T): 0
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVESTSPGREPVDTG
PPAPTVAPGPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 91-110

**Glycosaminoglycan attachment site.**

amino acids 44-47

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 116-119

**N-myristoylation site.**

amino acids 91-96

## **FIGURE 207**

GGCGGTTGGTGGTGC~~G~~CGCGCTGAAGGGTGTGGCGAGCAGCGTC~~T~~GGTTGCCGGCG  
 CGGGCCGGGACGGGCATGGCCCTGCTGCTGTGCC~~T~~GGTGTGCC~~T~~GTACGGCGCGCTGCCCA  
 CGGCTGTCTGC~~A~~CTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTACCGCCACCATGTGA  
 ACTTCAAGT~~C~~CTGGTGGGTGGCGACATCCCCGTGT~~C~~AGGGGCGCTGCTCACCGACTGGAGC  
 GACGACACGATGAAGGAGCTGCACCTGCCATCCCCGCCAAGATCACCCGGGAGAAGCTGGA  
 CCAAGTGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGAGAAGATGTACTTCC  
 CCGGTATTCCCCAACGAGCTGC~~A~~ACATCTCCGGGAGCAGGTGCACCTCATCCAGAAC  
 GCCATCATCGAAAGGCACCTGGCACCAGGCAGCTGGGGAGGGAGGGCAGCTCTCCAGGGAGGG  
 ACCCAGCCTAGCACCTGAAGGATCAATGCCATCACCCGCCGGGACCTCCCTAAGTAGCCC  
 CCAGAGGCGCTGGGAGTGTGCCACGCC~~T~~CCCTGAAGTTGCTCCATCTCACGCTGGGG  
 GTCAACCTGGGGACCCCTCCGCCATGGACACACATA~~C~~ATGAAAACCAGGCCGCAT  
 CGACTGTCAGCACCGCTGTGGCATCTTCAGTACGAGACC~~A~~TCC~~T~~GTCAACA~~A~~CTGCACAG  
 ACTCGCACGTGC~~C~~CTG~~T~~GGTATACTGCGAGTAGGGCTCAGGCATCACACCCACCGT  
 GCCAGGGCC~~T~~ACTGTCC~~T~~GGG~~T~~CC~~A~~GGCTCC~~T~~GGAGGGGCTCCGCC~~T~~CCAC  
 CTGGCTGT~~C~~ATCGGGTAGGGCGGGCGTGGTT~~C~~AGGGCGCACC~~A~~CTCCAAGC~~T~~GTGT  
 CCCACAGGT~~C~~TCGGCGAGTGAAGTCAGCTGTCCAGGGC~~T~~CTGA~~A~~CTACATAAAAC  
 TGGCACAA~~G~~TAA~~G~~TCC~~C~~CTCAAACCAACACAGGCAGTGTGTATGTGAGCAC~~T~~CGT  
 GGTGAGTATGTGGGGCACAGGCTGGCTCC~~T~~CAGCTCCACGT~~C~~CTAGAGGGCTCCGA  
 GGAGGTGGAACCTCAACCCAGCTCTGC~~G~~CAGGAGGC~~G~~GCTGCAGTC~~T~~TTCTCC~~T~~CAAAG  
 GTCTCCGACCC~~T~~CAGCTGGAGGC~~G~~G~~C~~ATCTTC~~T~~AAAGGGT~~C~~CCATAGGGTCTGGTTCC  
 ACCCCATCCCAGGTCTGTGGT~~C~~AGAGC~~T~~GGAGGGTCC~~T~~ACGATGGTTAGGGTGCC~~C~~  
 ATGGAGGGCTGACTGCC~~C~~ACATTGC~~T~~TCAGACAGGACACGAGCATGAGGTAAGGCCGC  
 CCTGACCTGGACTTCAGGGGAGGGG~~T~~AAAGGGAGAGAGGGAGGGGCTAGGGGT~~C~~CT  
 AGATCAGTGGGGCACTGCAGGTGGGCTCTCC~~T~~ATAC~~T~~GGACACCTGCTGGATGTCAC  
 CTCTGCAACCACACCC~~A~~GTGGTGGTT~~C~~ATGAACAGACCACGCT~~C~~CTGC~~T~~CTCC~~T~~GG  
 CCTGGGACACACAGAGCCACCCGCC~~T~~TGTGAGTGACCCAGAGAAGGGAGGC~~T~~CGGAGA  
 AGGGGTGCTGTAAGCCAACACCAGCGTGC~~G~~CGGCC~~T~~GCACACC~~T~~CGGACATCCCAGGC  
 ACGAGGGTGTGGATGTGGCACACATAGGACCACACGTCC~~C~~AGCTGGAGGAGAGGC~~T~~  
 GGGGCC~~C~~CCAGGGAGGGAGGCAGGGGTGGGGACATGGAGAGCTGAGGCAGC~~T~~CGTCTCC  
 CCGCAGCCTGGTATGCCAGC~~T~~TAAGGTGT~~C~~GGAGCCCCACACTGGCCAAC~~T~~GACCT  
 TGGAAGATGCTGCTGAGTGTCTCAAGCAGC~~A~~CTGACAGCAGCTGGG~~C~~CTGCC~~C~~AGGGCAAC  
 GTGGGGCGGAGACTCAGCTGGACAGCCC~~T~~GC~~T~~CACT~~T~~GGAGCTGGG~~C~~TGCTGCTGC  
 CTCAGGACCC~~C~~CTCCGCCACAGAGCTGAGCTGCCAGGGCAGGAGGGCGGGAGG  
 GAGGGAATGGGGTGGG~~C~~TGTGCGCAGCATCAGCGC~~T~~GGCAGGTCCG~~C~~AGAGCTGCC~~G~~  
 TGTGATTAAAGTCC~~T~~GAT~~T~~TTCTC

## **FIGURE 208**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399
><subunit 1 of 1, 157 aa, 1 stop
><MW: 17681, pI: 7.65, NX(S/T): 1
MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI
PVSGALLTDWSDDTMK
ELHLAIPIAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELRN
IREQVHЛИQNAIIER
HLAPGSWGGQLSREGPSLAPEGSMPSPRGDLP
```

**Signal peptide:**

amino acids 1-15

## **FIGURE 209**

AGCAGGAGCAGGAGAGGGACA**ATG**GAAGCTGCCCGTCCAGGTTCATGTTCTCTTATTCT  
 CCTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCCTG  
 GTGCTGCCAGGAACCCACGTGGCTCACAGATGTCCCAGCTGCCATGGAATTGCTGCC  
 ACTGAGGTGGCTGTCATAGGCTTCTTCAGGATTAGAAATACCAGCAGTGCCCCACTCCA  
 TAGCATGGTGCAAAAATTCCCAGGCGTGTCAATTGGATCAGCACTGATTCTGAGGTTCTGA  
 CACACTACAAACATCACTGGAACACCATCTGCCTCTTCGCCTGGTAGACAATGAACAACTG  
 AATTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTCATGAGAT  
 CAACAGCCTCCACATGGTGACAGAGTACAACCCCTGTGACTGTGATTGGTTATTCAACAGCG  
 TAATTTCAGATTTCATCTCCTCTGATAATGAACAAAGGCCTCCCCAGAGTATGAAGAGAACATG  
 CACAGATACCAGAAGGCAGCCAAGCTCTCCAGGGGAAGATTCTCTTATTCTGGTGGACAG  
 TGGTATGAAAGAAAATGGGAAGGGTGAATATCATTTCAAACTAAAGGAGTCTCAACTGCCAG  
 CTTTGGCAATTACCAGACTCTAGATGACGAGTGGATACACTGCCACAGCAGAAGTTCC  
 GTAGAGCATGTGCAAAACTTTGTGATGGATTCTTAAGTGGAAAATTGTTGAAAGAAAATCG  
 TGAATCAGAAGGAAAGACTCCAAAGGTGGAAC**TGA**CTTCTCCTGGAACTACATATGCC  
 AAGTATCTACTTTATGCAAAGTAAAAAGGCACAACACTCAAATCTCAGAGACACTAAACACAG  
 GATCACTAGGCCTGCCAACACACACACACGACGTGCACACACGCACGCACGGTGCACAC  
 ACACACGCGCACACACACACACAGAGCTTCATTCCTGTCTAAATCTGTTCTC  
 TTCTCCTCTTTAAATTTCATATCCTCACTCCCTATCCAATTCTCTTATCGTGCATT  
 CATACTCTGTAAGGCCATCTGTAACACACCTAGATCAAGGCTTAAGAGACTCACTGTGATG  
 CCTCTATGAAAGAGAGGCATTCTAGAGAAAGATTGTTCCAATTGTCATTAAATATCAAGT  
 TTGTATACTGCACATGACTTACACACAAACATAGTTCTGCTCTTAAAGGTTACCTAAGGGT  
 TGAAACTCTACCTCTTCATAAGCACATGTCCGTCTGACTCAGGATCAAAACCAAAGG  
 ATGGTTTAAACACCTTGTGAAATTGTCTTTGCCAGAAGTTAAAGGCTGTCTCCAAGTC  
 CCTGAACTCAGCAGAAATAGACCATGTGAAACTCCATGCTGGTTAGCATCTCCAACCTCC  
 TATGTAATCAACAACCTGCATAATAAATAAAGGCAATCATGTTATA

## **FIGURE 210**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401
><subunit 1 of 1, 273 aa, 1 stop
><MW: 30480, pI: 4.60, NX(S/T): 1
MEAAPSRFMILLFLLTCELAAEVAEEVEKSSDGPAGAAQEPTWLTDVPAAMEFIAATEVAVIG
FFQDLEIPAVPILHSMVQKFPGVSFGISTDSEVLTHYNITGNTICLFRLVDNEQLNLEDEDI
ESIDATKLSRFIEINSLHMVTEYNPVTIVIGLFNSVIQIHLLLIMNKASPEYEENMHRYQKAA
KLFQGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDEWDTLPTAEVSVEHVQNF
CDGFLSGKLLKENRESEGKTPKVEL
```

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 143-162

**FIGURE 211**

GGAGAGCCGGCTGGGACCGGAGTGGGGAGCGCGCGGTGGAGGTGCCACCCGGCGCGGGTG  
 GCGGAGAGATCAGAACGCCTCTTCCCCAAGCCGAGCCAACCTCAGCAGGGGACCCGGGCTCAGG  
 GACGCGGCGGGCGGGCGACTGCAGTGGCTGGACG**ATG**GCAGCGTCCGCCGGAGCCGGG  
 GCGGTGATTGCAGCCCCAGACAGCCGGCGCTGGCTGTGGTCGGTGCCTGGCGGGCGCTTGG  
 GCTCTTGACAGCTGGAGTATCAGCCTGGAAGTATATACGCCAAAGAAATCTCGTGGCAA  
 ATGGTACACAAGGGAAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACC  
 TCAGTCTCCTGGAGCTTCCAGCCAGAGGGGGCGACACTACTGTGTCGTTTCCACTACTC  
 CCAAGGGCAAGTGTACCTGGATTATCCACCATTAAAGACAGAACATCAGCTGGCTGGAG  
 ACCTTGACAAGAAAGATGCATCAATCACATAGAAAATATGCAGTTATACACAATGGCACC  
 TATATCTGTGATGTCAAAACCCCTCTGACATCGTGTCCAGCCTGGACACATTAGGCTCTA  
 TGTCGTAGAAAAAGAGAATTCGCTGTGTTCCAGTTGGTAGTGGTGGGCATAAGTTACTG  
 CTGTGGCCTAGGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCCCTATAGAAGGAAA  
 AACTCTAAACGGGATTACACTGGCTGCAGTACATCAGAGAGTTGTACCAGTTAACGAGGC  
 TCCTCGGAAGTCCCCCTCCGACACTGAGGGTCTTGTAAAGAGTCTGCCTCTGGATCTCACC  
 AGGGCCCAGTCATATATGCACAGTTAGACCCTCCGGCGGACATCACAGTGACAAGATTAAC  
 AAGTCAGAGTCTGTGGTGTGCGGATATCCGAAAGAAT**TAA**GAGAACATACAGAACATATC  
 CTCAGCAAGAAACAAAACCAACTGGACTCTCGTGCAGAAAATGTAGCCCATTACCACATGT  
 AGCCTGGAGACCCAGGCAAGGACAAGTACACGTACTCACAGAGGGAGAGAAAGATGTGT  
 ACAAAAGGATATGTATAAATATTCTATTAGTCATCCTGATATGAGGAGCCAGTGTGCATGA  
 TGAAAAGATGGTATGATTCTACATATGTACCCATTGTCTGCTGTTGTACTTCTTTTC  
 AGGTCAATTACAATTGGGAGATTTCAGAAACATTCCCTTCACCATCATTAGAAATGGTTG  
 CCTTAATGGAGACAATAGCAGATCCTGTAGTATTCCAGTAGACATGGCCTTTAATCTAAG  
 GGCTTAAGACTGATTAGTCTTAGCATTACTGTAGTTGGAGGATGGAGATGCTATGATGGAA  
 GCATACCCAGGGTGGCCTTACAGTACGATTCAGTACCTTATTGTCTGCCGCTTTAAAA  
 AATACCCATTGGCTATGCCACTTGAAAACAATTGAGAAGTTTTGAAGTTTCTCACT  
 AAAATATGGGCAATTGTTAGCCTTACATGTTGTAGACTTACTTAAGTTGCACCCCTG  
 AAATGTGTATCAATTCTGGATTCAATAGCAAGATTAGCAAAGGATAATGCCAAG  
 GTCACTTCATTCTGGACACAGTTGGATCAACTAGTAAAGTAGAAAATCCAAGCTTGCTT  
 GAGAACTTTGTAACGTGGAGAGTAAAAGTATCGGTTTA

**FIGURE 212**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510
><subunit 1 of 1, 269 aa, 1 stop
><MW: 29082, pI: 9.02, NX(S/T): 3
MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKST
TSTTGGLTSVWSFQPEGADTTVSFFHYSQGQVYLGNYPFFKDRISWAGDLDKKDASINEN
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVVVGIVTAVVLGLTLISMI
LAVLYRRKNSKRDYTGCSTSESLSPVKQAPRKSPSDTEGLVKSLSHGPVIYAQLDHSG
GHHSINKSESVVYADIRKN
```

**Signal peptide:**

amino acids 1-37

**Transmembrane domain:**

amino acids 161-183

## **FIGURE 213**

GCCGGCTGTGCAGAGACGCC **ATG**TACCGGCTCCTGTCAGCAGTGACTGCCCGGGCTGCCGCC  
 CCCGGGGCTTGGCCTCAAGCTGGGACGACGCCGGTCCATCAGCGGCCGGCTGCCGCC  
 TCTCGGCCACGGCTGGGCTGGGCTCGGGCTGGGCTGGGCTGGCGCTGGGTGAAGC  
 TGGCAGGTGGGCTGAGGGCGCGGCCCGCAGTCCCCCGGGCCCCGACCCTGAGGCG  
 TCGCCTCTGGCCGAGCCGCACAGGAGCAGTCCCTGCCCGTGGTCTCCGAGACCCGGC  
 GCCGCCCTGCTCCAGGTGCTGCCAGAGCCATCGAGAGCAGCCGCACCTGCTGCACAGGA  
 TCAAGGATGAGGTGGGCGCACCGGCATACTGGTTGGAGTTCTGTAGATGGAAAAGAAGTC  
 TGGTCAGAAGGTTAGGTTATGCTGATGTTGAGAACCGTGACCATGTAACACCAGAGACAGT  
 TATGCGAATTGCTAGCATCAGAAAAGTCACCATGGTTGCTCTGCCAAATTGTGGGAAG  
 CAGGGAAACTGGATCTTGATATTCCAGTACAACATTATGTTCCCAGTAAAGAAAAAGAA  
 TATGAAGGTGAAAAGGTTCTGTACAACAAGATTACTGATTCCCATTAAAGCCTGAAGATGA  
 TCATTATGAAAAGGACATAAAAAGGTGAAAGAAGAGAAAGCTTATAAAGCCTGAAGATGA  
 TGAAAGAGAATGTTGCATTGAGCAAGAAAAGAAGGCAAAGTAATGAAAAGAATGATT  
 ACTAAATTAAAACAGAGCAGGAGAATGAAGCCAATGCCGAATTCAAAACCTGGCAAGAA  
 AAAGAATGATTGAAACAAGGCGAATTATATTGAGAGAAAAGTTGAAAATTCAATTGAAT  
 CCCTAACGATTATTAAAAATGATCCTTGTCTTCAAACCTGGTAGTCAGTTTGATTCA  
 ACTTTGGCTATACCCTACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAAATATTGGA  
 CTATATGCAGAAAATATTCCATGACTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGC  
 CAGTGATTACAATAGAGCAAGG**TAA**ATGAATACTTCTGCTGTCTAGCTATATCGCATC  
 TTAACACTATTATTAAATTAAAAGTCAAATTTCATTGTTCCATTCAAATCAACCTGC  
 CACATTGGAGCTTCTACATGTCTGTTCTCATCTGTAAAGTGAAGGAAGTAAACA  
 TGTTTATAAAGTAAAAAA

**FIGURE 214**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522
><subunit 1 of 1, 373 aa, 1 stop
><MW: 41221, pI: 8.54, NX(S/T): 0
MYRLLSAVTARAAAPGGGLASSCGRRGVHQAGLPPLGHGWVGGLGLGLALGVLAGGLRG
AAPAQSPAAPDPEASPLAEPPEQSLAPWSPQTAPPSCRCFARAIESSRDLLHRIKDEVGA
PGIVVGVSVDGKEVWSEGLGYADVENRVPCKPETVMRIASISKSLSLTVALAKLWEAGKLDLD
IPVQHYVPEFPEKEYEGEKVSVTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF
EQEKEGKSNEKNDFTKFKTEQENEAKCRNSKPGKKNDFEQGELYLREKFENSIESRLFKN
DPLFFKPGSQFLYSTFGYTLLAAIVERASGCKYLDYMQKIFHDLDMLTTVQEENEPVIYNRAR
```

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 39-60

## **FIGURE 215**

GTGACACTATAGAAGAGCTATGACGTCGCATGCACCGTACGTAAGCTCGGAATTGGCTCG  
 AGGCTGGTGGGAAGAACGCCGAG**ATG**CGCCAGCCAGCGCTGGGCAACCCGGCTGCTCCTGC  
 TCTTGCTGATGGCGGTAGCAGCGCCAGTCGAGGCCGGGCAGCGGCTGCCGGCCGGACT  
 GGTGCGCGAGGGCTGGGCGGAAGGTCGAGAGGGCGAGGCCTGTGGCACGGTGGGCTGCT  
 GCTGGAGCACTCATTTGAGATCGATGACAGTGCCAACCTCCGGAAAGCGGGCTCACTGCTCT  
 GGAACCAGCAGGATGGTACCTTGTCCCTGTCACAGCGCAGCTCAGCGAGGAGGAGCGGGC  
 CGACTCCGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCCCAAGGCGACCCGG  
 GGCCCTGGATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTGTCCCTGCGTGTCCCTGG  
 TGGAGTCGCACCTGTCGGACCAGCTGACCCCTGCACGTGGATGTGGCCGGAACGTGGTGGC  
 GTGTCGGTGGTACGCACCCGGGGCTGCCGGGCCATGAGGTGGAGGACGTGGACCTGGA  
 GCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCACACAGCCCCAGGCCCTGAGACGGCGG  
 CCTTCATTGAGCGCCTGGAGATGGAACAGGCCAGAAGGCCAAGAACCCCCAGGAGCAGAAG  
 TCCTTCTCGCAAATACTGGATGTACATCATTCCGTCGTCCCTGTTCCCTCATGATGTCAGG  
 AGCGCCAGACACCAGGGGCCAGGGTGGGGTGGGGGTGGTGGTAGTGGCC  
 TTTGCTGTGTGCCACCCCTCCCTG**TAA**GTCTATTTAAAAACATCGACGATACTGAAATGTG  
 TGAACGTTTGAAAAGCTACAGCTTCCAGCAGCCAAAGCAACTGTTGTTGGCAAGACGG  
 TCCTGATGTACAAGCTTGATTGAAATTCACTGCTACTTGATACTGTTATTGAGAAACCCAAG  
 GAATGGCTGTCCCCATCCTCATGTGGCTGTGGAGCTCAGCTGTGTTGTGGCAGTTAT  
 TAAACTGTCCCCAGATCGACACGAAAAAAAAAA

## **FIGURE 216**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529
><subunit 1 of 1, 269 aa, 1 stop
><MW: 28004, pI: 5.80, NX(S/T): 1
MAAASAGATRLLLLLMAVAAPSRARGSGCRAVTGARGAGAEGREGEACGTVGLLLEHSFEI
DDSANFRKRGSSLWNQQDGTLSLSQRQLSEEERGLRDVAALNGLYRV RIPRRPGALDGLEA
GGYVSSFVPACSLVESHLSDQTLHVDVAGNVGVSVVTHPGGCRGHEVEDVDLELFNTSVQ
LQPPTTAPGPETAAFIERLEMEQAQKAKNPQEOKSFFAKYWMYII PVVLFLMMMSGAPDTGGQ
GGGGGGGGGGGGSGLCCVPPSL
```

**Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 226-243

**FIGURE 217**

GGAGCGCTGCTGGAACCCGAGCCGGAGCCGGAGCACAGCAGGGAGGGTGGCCTGGCGGCCT  
 GGAGCCGGACGTGTCCGGGGCGTCCCCGCAGACCGGGGCAGCAGGTGTCCTGGGGCTGGAACT  
**ATG**CTGGTGACTGCCTACCTGCTTTGTAGGCCTCCTGGCCTCCTGCCTGGGGCTGGAACT  
 GTCAAGATGCCGGCTAAACCCCTGGAAGGGCCTGCAGCAATCCCTCCTCGGTTTC  
 AACTGGACTTCTATCAGGTCTACTCCTGGCCCTGGCAGCTGATTGGCTTCAGGCCCCCTAC  
 CTCTATAAACTCTACCAGCATTACTACTTCCTGGAAGGTCAAATTGCCATCCTCTATGTCTG  
 TGGCCTTGCCTCTACAGTCTTGGCTAGTGGCCTCCTCCCTGTGGATTGGCTGGTC  
 GCAAGAATTCTTGTGCTCTTCTCCCTGACTTACTCACTATGCTGCTTAACCAAACCTCT  
 CAAGACTACTTGTGCTGCTAGTGGGGCGAGCACTGGTGGCTGTCCACAGCCCTGCTCT  
 CTCAGCCTTCGAGGCCTGGTATATCCATGAGCACGTGGAACGGCATGACTCCCTGCTGAGT  
 GGATCCCAGCTACCTTGCTCGAGCTGCCTCTGGAACCATGTGCTGGCTGTAGTGGCAGGT  
 GTGGCAGCTGAGGCTGTAGCCAGCTGGATAGGGCTGGGCCTGTAGGCCCTTGTGGCTGC  
 CATCCCTCTGGCTCTGGCAGGGCCTTGGCCCTCGAAACTGGGGGAGAACTATGACC  
 GGCAGCGTGCCTCTCAAGGACCTGTGCTGGAGGCCTGCGCTGCCTCTGCGACCGCCGC  
 GTGCTGCTGCTGGCACCATACAAGCTCTATTGAGAGTGTCACTTCATCTTGTCTCCT  
 CTGGACACCTGTGCTGGACCCACACGGGGCCCTCTGGCATTATCTCCAGCTTCATGG  
 CAGCCAGCCTGCTGGCTTCCCTGTACCGTATGCCACCTCCAAGAGGTACCACCTCAG  
 CCCATGCACCTGCTGTCCCTGCTGCTCATCGTCGTTCTCTCTCATGTTGACTTT  
 CTCTACCAGCCCAGGCCAGGAGAGTCCGGTGGAGTCCTCATAGCCTTCTACTTATTGAGT  
 TGGCTTGTGGATTATACTTCCAGCATGAGCTCCTACGGAGAAAGGTGATCCCTGAGACA  
 GAGCAGGGCTGGTACTCAACTGGTCCGGTACCTCTGCACTCACTGGCTGCCTAGGGCT  
 CCTTGTCCCTCATGACAGTGATCGAAAAACAGGCAGTCGAATATGTTCAGCATTGCTCTG  
 CTGTCATGGTGTGGCTCTGCTGGCAGTGGTGGACTCTTACCGTGGTAAGGCATGATGCT  
 GAGCTGCGGGTACCTCACCTACTGAGGAGCCATGCCCTGAGCTG**TAA**CCCCACTCCAG  
 GACAAGATAGCTGGGACAGACTCTGAATTCCAGCTATCCGGGATTGTACAGATCTCTGT  
 GACTGACTTTGTGACTGTCTGTGGTTCTCCTGCCATTGCTTGTGTTGGAGGACATGA  
 TGGGGGTGATGGACTGGAAAGAAGGTGCCAAAGTCCCTCTGTGTTACTCCCATTAGAAA  
 ATAAACACTTTAAATGATCAAAAAAAAAAA

## **FIGURE 218**

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPY  
LYKLYQHYYFLEGQIAILYVCGLASTVLFGIVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS  
QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARA\_AFWNHVLA  
VAEAEVASWIGLGPVAPFVAAIPLLALAGALALRNWGENYDRQRAFSRTCA  
GGLRCLLSDRRVLLLGTIQALFESVIFIFVFLWPVLDPHGAPLGII  
FSSFMAASLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTF  
STSPGQESPVESFIAFLIELACGLYFPSMSFLRRKV  
PETEQAGVLNWFRVPLHSLACLGLLVLHDSDRKTGTRNMFSICSA  
VMVMALLAVVGLFTVV  
RHDAELRVPSPTEEPYAPEL

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,  
314-330, 343-359, 379-394, 410-430

**FIGURE 219**

GCGACGCGCGGGCGGGCGAGAGGAAACGCGGCCGGCCGGCCCTGGAG**ATG**  
GTCCCCGGCGCCGGCTGGTGTCTCGTGCCTGGCTCCCCCGTGCCTCGCGCCA  
CGGCTTCCGTATCCATGATTATTGTACTTCAAGTGCTGAGTCCTGGGACATTGATA  
TCTTCACAGCCACACCTGCCAAGGACTTGGTGGTATCTTCACACAAGGTATGAGCAGATT  
CACCTTGTCCCCGCTGAACCTCCAGAGGCCTGCAGGGAACTCAGCAACGGTTCTCATCCA  
GGACCAGATTGCTCTGGTGGAGAGGGGGGCTGCTCCTCTCCAAGACTCGGGTGGTCC  
AGGAGCACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTAC  
GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTTCCTGCTCGG  
CCGAGACGGCTACATGATCCGCCCTCTGGAACAGCATGGCTGCCATGGCCATCATT  
CCATCCCAGTCAATGTCACCAGCATCCCCACCTTGAGCTGCTGCAACCGCCCTGGACCTTC  
TGG**TAGA**AAGAGTTGTCCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGAAACCC  
AGGAATTTGCTACTTGAATTGGAGATAGCATCTGGGACAAGTGGAGCCAGGTAGAGGA  
AAAGGGTTGGCGTTGCTAGGCTGAAAGGGAACACCACGGCCTCCCTCCCCAGG  
GCCCCAAGGGTCTCATGCTACAAGAACAGAGGCAAGAGACAGGCCAGGGCTCTGGCTA  
GAACCCGAAACAAAAGGAGCTGAAGGCAGGTGGCTGAGGCCATCTGTGACCTGTCACACT  
CACCTGGCTCCAGCCTCCCCACCCAGGGCTCTGCACAGTGACCTCACAGCAGTTGG  
AGTGGTTAAAGAGCTGGTGTGGGACTCAATAAACCTCACTGACTTTAGCAATAAA  
GCTTCTCATCAGGGTTGCAAAAAAAAAAAAAAA

## **FIGURE 220**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532
><subunit 1 of 1, 188 aa, 1 stop
><MW: 21042, pI: 5.36, NX(S/T): 2
MVPGAAGWCCLVLWLPACVAAHGFRRIHDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ
IHLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDNAVDNDSF
YVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW
```

**Signal peptide:**

amino acids 1-20

**FIGURE 221**

TCTGCCTCCACTGCTCTGTGCTGGGATC**ATG**GAACCTGCACTGCTGTGGCTGGTGGTGA  
TGGCTGGTGTATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTG  
ACTGGGAAAATGCCCATCCTCTCCTACTGGCCCTACGGCTGTCAGTGCAGACTAGGTGGCAG  
AGGCCAACCAAAGATGCCACGGACTGGTGTGCCAGACCCATGACTGCTGCTATGACCACC  
TGAAGACCCAGGGTGCAGCATCTACAAGGACAACAACAAAGCAGCATACTTGTATGGAT  
TTATCTCAACGCTATTGTTAATGGCTGTGTTAATGTGATCTATCTGGAAAATGAGGACTC  
CGAA**TAA**AAAGCTATTACTAWTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAA

## **FIGURE 222**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538
><subunit 1 of 1, 116 aa, 1 stop
><MW: 12910, pI: 6.41, NX(S/T): 1
MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDW
CCQTHDCCYDHLKTQGCGIYKDNNKSSIHCMDLSQRYCLMAVFNVVIYLENEDSE
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 1-24

**N-glycosylation site.**

amino acids 86-89

**N-myristoylation sites.**

amino acids 20-25, 45-50

**Phospholipase A2 histidine active site.**

amino acids 63-70

**FIGURE 223**

CTCGCTTCTTCCTCTGGATGGGGGCCAGGGGCCAGGAGAGTATAAGGCATGTGGAG  
GGTGCCCGACAACCAAGACGCCAGTCACAGGCCAGAGCCCTGGG**ATG**CACCGGCCAGAGG  
CCATGCTGCTGCTCACGCTGCCCTCCTGGGGGCCACCTGGCAGGAAAGATGTAT  
GGCCCTGGAGGAGGCAAGTATTTCAGCACCCTGAAGACTACGACCATGAAATCACAGGGCT  
GCGGGTGTCTGTAGGTCTTCCTGGTAAAAAGTGTCCAGGTGAAACTGGAGACTCCTGGG  
ACGTGAAACTGGGAGCCTAGGTGGAAATACCCAGGAAGTCACCCCTGCAGCCAGGCGAATAC  
ATCACAAAAGTCTTGTGCCTCCAAGCTTCCTCCGGGTATGGTCATGTACACCAGCAA  
GGACCGCTATTCTATTGGAAAGCTTGATGCCAGATCTCCTCTGCCTACCCCAGCCAAG  
AGGGGCAGGTGCTGGTGGCATTCTATGCCAGTATCAACTCCTGGCATCAAGAGCATTGGC  
TTTGAATGGAATTATCCACTAGAGGGAGCCGACCACTGAGCCACCACTTAATCTCACATACTC  
AGCAAACTCACCCGTGGTCGC**TAG**GGTGGGTATGGGCCATCCGAGCTGAGGCCATCTGT  
GTGGTGGTGGCTGATGGTACTGGAGTAACTGAGTCGGACGCTGAATCTGAATCCACCAATA  
AATAAAAGCTTCTGCAGAAAA

## **FIGURE 224**

```
></usr/seqdb2/sst/DNA/Dnaseqs:min/ss.DNA76541
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19600, pI: 5.89, NX(S/T): 1
MHRPEAMLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSGLLLKVSVQVK
LGDSWDVKLGALGGNTQEVTLQPGEYITKVFVAFQAFLRGMVMYTSKDRYFYFGKLDGQISS
AYPSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYSANSPVGR
```

**Signal peptide:**

amino acids 1-22

## **FIGURE 225**

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTCTGGGCTCCAACGCAGCTCTGTGGCT  
 GAACTGGGTGCTCATCACGGGAAC TGCTGGCTATGGAATACAGATGTGGCAGCTCAGGTAG  
 CCCCAAATTGCCTGGAAGAATA CATCATGTTTCGATAAGAAGAAATTGTAGGATCCAGTT  
 TTTTTTTAACCGCCCCCTCCCACCCCCAAAAAAACTGTAAAGATGCAAAACGTAATAT  
 CCATGAAGATCCTATTACCTAGGAAGATTGATGTTGCTGCGAATGCGGTGTTGGGATT  
 TATTGTTCTGGAGTGTCTGCGTGGCTGGCAAGAATAATGTTCAAATCGGTCCATCT  
 CCCAAGGGGCTCAATTTCCTGGGTGTCAGCGAGCCCTGACTCACTACAGTGCAGCTG  
 ACAGGGGCTGTCACTGCAACTGGCCCTAAGCCAAGACCTAAGGACGACCTTGAA  
 CAATACAAAGGATGGTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTT  
 ATAGCCCCACTGTCTACTGACAATGCTTCTTGC CGAACGAGGATGCCCTAAGGGCTG  
 TAGGTGTGAAGGCAAAATGGTATATTGTAATCTCAGAAATTACAGGAGATA CCTCAAGTA  
 TATCTGCTGGTTGCTTAGGTTGTCCTCGCTATAACAGCCTTCAAAAACTTAAGTATAAT  
 CAATTAAAGGGCTCAACCAGCTCACCTGGCTATACTGACCATAACCATA CAGCAATAT  
 TGACGAAAATGCTTTAATGGAATACG CAGACTCAAAGAGCTGATTCTAGTTCAATAGAA  
 TCTCCTATTTCTTAACAATACCTTCAGACCTGTGACAAATTACGAAACTTGGATCTGTCC  
 TATAATCAGCTGCATTCTGGGATCTGAACAGTTGGGCTTGCGGAAGCTGCTGAGTT  
 ACATTACGGTCTA ACTCCCTGAGAACCATCCCTGTGCGAATATTCCAAGACTGCCGCAACC  
 TGGAACTTTGGACCTGGGATATAACCGGATCCGAAAGTTAGCCAGGAATGTC TTGCTGGC  
 ATGATCAGACTCAAAGAAC TT CACCTGGAGCACAATCAATTTCAGCTCAACCTGGCCCT  
 TTTCCAAGGTGGTCAGCCTCAGAACCTTACTTGCA GTGGAATAAAATCAGTGTCA TAG  
 GACAGACC ATGTCCTGGACCTGGAGCTCCTTACAAAGGCTGATTATCAGGCAATGAGATC  
 GAAGCTTCAGTGGACCCAGTGTGTTCCAGTGTGCCCAGTGTGAGCTCAACCTGGG  
 TTCCAACAAGCTCACATTATTGGTCAAGAGATTGGATTCTGGATATCCCTCAATGACA  
 TCAGTCTGCTGGGAATATGGGAATGCA GCAGAACATATTGCTCCCTGTAAGACTGGCTG  
 AAAAGTTAAAGGTCTAAGGGAGAATACAATTATCTGTGCCAGTCCAAAGAGCTGCAAGG  
 AGTAAATGTGATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAAGTACTACAGAGAGGT  
 TTGATCTGCCAGGGCTCTCCAAAAGCCGACGTTAAGCCCAGCTCCCCAGGCCGAAGCAT  
 GAGAGCAAACCCCTTGCCCCCGACGGTGGGAGCCACAGAGCCGCCAGAGACCGATGC  
 TGACGCCGAGCACATCTTTCCATAAAATCATCGCGGGCAGCGTGGCGTTTCCTGTCCG  
 TGCTCGTCATCCTGCTGGTTATCTACGTGTCA TGGAAGCGGTACCCCTGCGAGCATGAAGCAG  
 CTGCAGCGCCTCCCATGCGAAGGCACAGGAAAAGAAAAGACAGTCCCTAAAGCAAAT  
 GACTCCCAGCACCCAGGAATTATGTAGATTATAACCCACCAACACGGAGACCAGCGAGA  
 TGCTGCTGAATGGGACGGGACCCCTGCACCTATAACAAATGGGCTCCAGGGAGTGTGAGGTA  
TGA ACCATTGTGATAAAAAGAGCTCTTAAAGCTGGGAATAAGTGGTGTGTTATTGAACTC  
 TGGTGA CTATCAAGGGAACCGCGATGCCCTCCCTCCCTCTCCCTCACTTGGTGG  
 CAAGATCCTCCTGTCGTTAGTGCATTCAATAACTGGTCATTTCCTCTCATACATA  
 ATCAACCCATTGAAATTAAATACCACAAATCAATGTGAAGCTGAACTCCGGTTAATATAA  
 TACCTATTGTATAAGACCTTACTGATTCCATTAAATGTCGCATTGTTAAGATAAAACT  
 TCTTCATAGGTAAAAAAAAAA

**FIGURE 226**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301
><subunit 1 of 1, 513 aa, 1 stop
><MW: 58266, pI: 9.84, NX(S/T): 4
MGFN VIRLLSGSAVALVIAPTVLLTMLSSAERGCPKGCRCEGK MVYCESQKLQEIPSSISAG
CLGLSL RYNSLQKLKYNQFKGLNQLTWLYLDHNHISNIDENAFNGIRRLKELILSSNRISYF
LNNTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRTIPVRI FQDCRNLELL
DLGYNRIRSLARNVFAGMIRLKELHLEHNQFSKLNLA F PRLVSLQONLYLQWNKISVIGQTM
SWTWSSLQR LDLSGNEIEAFSGPSVFQCVPNLQRLNLD SNKLTFIGQEILD SWISLNDISLA
GNIWECSRNICSLVNWLKSFKGLRENTIICASPKE LQGVNVIDAVKNYSICGKSTTERFDLA
RALPKPTFKPKLPRPKHESKPPLPPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLVI
LLVIYVSWKRYPASMKQLQQRSLMRRHRKKKRQSLKQMTPSTQE FYVDYKPTNTETSEMLLN
GTGPCTYNKSGSRECEV
```

**Important features of the protein:****Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 420-442

**N-glycosylation sites.**

amino acids 126-129, 357-360, 496-499, 504-507

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 465-468

**Tyrosine kinase phosphorylation site.**

amino acids 136-142

**N-myristoylation sites.**

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

**FIGURE 227**

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCACTATCCTAAGTTGACTGTCCTT  
 TAAATATGTCAAGATCCAGACTTTCAGTGTACCTCAGCGATCTAACGATAGGGATCTG  
 TGTTGCCGCTATTCCAGTTGGTGCTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGT  
 AAATTATAATGACCAACACCCTAATGGCTGGTATATCTGGATCCTCTGCTGCTGGTTTGG  
 TGGCAGCTCTCTGTGGAGCTGTGGCCTCTGCCTCCAGTGCTGGCTGAGGAGACCCCGA  
 ATTGATTCTCACAGGCCACCATGGCAGTTTGCTGTTGGAGACTGGACTCTATTATGG  
 GACAGAAGCAGCTGTGAGTCCAATGTTGAATTACACCTCAAACCTCAAACCCCTGACCTAT  
 ATCCTGTTCTGCTCCATGTTGGCCCTTAGGCTCCCCACCTCCATATGAAGAAATTGTA  
 AAAACAACCTGATTTTAGGTGTGGATTATCAATTAAAGTATTAACGACATCTGTAATTCCA  
 AAACATCAAATTAGGAATAGTTATTCAGTTGGAAATGTCCAGAGATCTATTATATA  
 GTCTGAGGAAGGACAATTGACAAAAGAATGGATGTTGGAAAAAATTTGGTCATGGAGATG  
 TTTAAATAGTAAAGTAGCAGGCTTGATGTGCACTGCTGTATCATACTTTATGCTACAC  
 AACCAAATTAATGCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTT  
 TCCATCACATTAGGACTCCACTGCAGTATACAGCACACCATTCTGCTTAAACTCTTC  
 CTAGCATGGGTCCATAAAATTATTATAATTAAACAATAGCCCAAGCCGAGAATCCAACAT  
 GTCCAGAACCGAGAACCGAGAAAGATAGTATTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAA  
 GAAAAGTTGGAGTTGAAGGGTAAAGGATAATGAAGAGGAAAAGGAAAAGATTACAAGTCT  
 CAGCAAAAACAAGAGGTTTATGCCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGA  
 AGGAGATTGCTGAAGATATAGAGCACATATAATGCCAACACGGGGAGAAAAGAAAATTCCC  
 CTTTACAGTAATGAATGTGGCCTCCATAGTCCATAGTGTCTCTGGAGCCTCAGGGCTG  
 GCATTATTGCAGCATCATGCTAACGACCTTCGGCATAGGTATCTGTTCCATGAGGACTGC  
 AGAAAGTAGCAATGAGACATCTCAAGTGGCATTGGCAGTGGCCATCAGCAGGGGGACAGA  
 CAAAAACATCCATCACAGATGACATATGATCTCAGCTGACAAATTGTTGAACAAAACAAT  
 AACATCAATAGATATCTAAAAA

## **FIGURE 228**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303
><subunit 1 of 1, 146 aa, 1 stop
><MW: 16116, pI: 4.99, NX(S/T): 0
MSRSRLFSVTSAISTIGILCLPLFQLVLSDLPCEEDEMCSVNYNDQHPNGWYIWILLLVLA
ALLCGAVVLCLQCWLRRPRIDSHRRTMAVFAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYP
VPAPCFGPLGSPPPYEEIVKTT
```

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 52-70

**FIGURE 229**

GAGCGGAGTAAATCTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCCACCGGGGT  
 TTCTCCAGCTCGATCTGGAGGCTGCCAGTGTGGACGCAGCTGACGCCGCTTATT  
 GCTCTCGCTCGCTGCCCGCAGAAGCTCCGTGGCGCGACCGTGACGAGAACCC  
 ACGGCCAGCTCAGTTCTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCTTTAAACT  
 CCCTCTCAAAACTCATCTCTGGGTGACTGAGTTAATAGAGTGGATACAACCTGCTGAAG  
 ATGAAGAATATAAATATTGAGGATATTTTTCTTTTTCAAGTCTTGATTGTGGC  
 TTACCTCAAGTTACCATTTCAGTCAGTCTGTTGTTGCTTCTCAGAA**ATG**TTTTTA  
 CAATCTCAAGAAAAAATATGTCCCAGAAATTGAGTTACTGTTGCTGTATTGGACTCATT  
 TGGGGATTGATGTTACTGCACTATACTTTCAACAAACCAAGACATCAAAGCAGTGTCAAGTT  
 ACGTGAGCAAATACTAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAAATAAGA  
 ACACAGTGGATGTCGAGAACGGTGTCTATGGCAGGATATGCGGATCTGAAAAGAACAAATT  
 GCTGTCCTCTGGATGACATTTGCAACGATTGGTGAAGCTGGAGAACAAAGTTGACTATAT  
 TGTTGTGAATGGCTCAGCAGCCAACACCAATGGTACTAGTGGGAATTGGTGCAGTAA  
 CCACAAATAAAAGAACGAATGTCTGGGCAGTATCAGA**TAG**CAGTTGAAAATCACCTTGTGC  
 TGCTCCATCCACTGTGGATTATATCCTATGGCAGAAAAGCTTATAATTGCTGGCTTAGGAC  
 AGAGCAATAACTTTACAATAAAAGCTCTACACATTTCAAGGAGTATGCTGGATTATGGAAC  
 TCTAATTCTGTACATAAAATTTAAAGTTATTGTTGCTTCAGGCAAGTCTGTTCAATG  
 CTGTAATGTCCTTAAAGAGAATTGGTAACTGGTTGATGTGGTAAGCAGATAGGTGAGT  
 TTTGTATAATCTTTGTGTTGAGATCAAGCTGAAATGAAAACACTGAAAACATGGATTC  
 ATTTCTATAACACATTAAAGTATATAACACGTTTTGGACAAGTGAAGAATGTTAA  
 TCATTCTGTCAATTGTTCTCAATAGATGTAAGTACTGTTAGACTACGGCTATTGAAAAAATGTG  
 CTTATTGTAATATTGTTATTCCAATTATGAGCAGAGAAAAGGAAATAATGTTGAAA  
 TAATGTTTGAATCATGACCCAAAGAATGTATTGACTATCCTCAGAATAACTGA  
 AGGTTAATTATTGTATATTAAAATTACACTTATAAGAGTATAATTGAAATGGTAG  
 CAGCCACTGTCCATTACCTATGTAACATTGGGCAATTAAACAGCATTAAATAGTT  
 GTAAAATCTAACTTATACATTGAGAATAAAAGATATTGATGAGAGTAACAATA  
 AAGTATTGATTTCACATACATGAATGTCATTAAAGTTAATCCTTGAGTGTCT  
 ATGCTATCAGGAAAGCACATTATTCCATATTGGGTAATTGCTTTATTATATTGGTC  
 TAGGAGGAAGGGACTTGGAGAATGAACTCTTGAGGACTTAGCCAGGTGTATAATAAA  
 GGTACTTTGTGCTGATTAAATTGCTGGAAAGTGTAAACATTATATTATAAGAGTATC  
 CTTTATGAAATTGTAACAGATGCAATTGAGTATTGCTTATATTATAATGCCAC  
 TTAAAATAAGAACATTAAATATAAACTATGAAGATTGACTATCTTTCAGGAAAAAGCT  
 GTATATAGCACAGGAAACCTAATCTGGGTAAATTCTAGTATAAAACAAATTATACTTTAT  
 TTAAATTTCCCTGTAGCAAATCTAATTGCCACATGGTGCCTATATTGATGAGTATT  
 CTCTATAGTAATGCTTAAGTGCAGCTAGCTTAGATTTAGACTATAGAATTAGATAT  
 TGTATTGTTCGTCATTATAATATGCTACCACATGTAGCAATAATTACAATATTGTTATTAAA  
 TAAATATGTGAAATATTGTTCATGAAAGACAGATTCCAATCTCTTCTCTGTA  
 CTGTCTACCTTATGTGAAGAAATTAATTATGCCATTGCCAGGT

## **FIGURE 230**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648
><subunit 1 of 1, 140 aa, 1 stop
><MW: 15668, pI: 10.14, NX(S/T): 5
MFFTISRKNMSQKLSLLLLVFGЛИWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE
ENKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNL
VPVTTNKRTNVSGSIR
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

## **FIGURE 231**

CGCGGGCCGGGCCGGGGTGAGCGTGCCGAGGCGGCTGTGGCGCAGGCTTCCAGCCCCCAC  
**CATG**CCGTGGCCCCTGCTGCTGCTGGCCGTGAGTGGGGCCCAGACAAACCGGCCATGCT  
 TCCCCGGGTGCCAATGCAGGGTGGAGACCTTCGGGCTTTGACAGCTTCAGCCTGACTCGG  
 GTGGATTGTAGCGGCCTGGGCCCCACATCATGCCGGTGCCCATCCCTCTGGACACAGCCC  
 CTTGGACCTGTCCCTCCAACCAGCTGGAGATGGTGAATGAGTCGGTGTGGCGGGCCGGCT  
 ACACGACGTTGGCTGGCCTGGATCTCAGGCCACAACCTGCTCACAGCATCTCACCCACTGCC  
 TTCTCCCGCCTCGCTACCTGGAGTCGCTGACCTCAGCCACAATGGCCTGACAGCCCTGCC  
 AGCGAGAGCTTCACCAGCTCACCCCTGAGCGACGTGAACCTTAGCCACAACCAGCTCCGG  
 AGGTCTCAGTGTCTGCCTCACGACGCACAGTCAGGGCGGGCACTACACGTGGACCTCTCC  
 CACAACCTCATTCACCGCCTCGTCCCCACCCACGAGGGCGGCCGCCTGCCTGCGCCCACCC  
 TCAGAGCCTGAACCTGGCCTGGAACCGGCTCCATGCCGTGCCAACCTCCGAGACTTGGCC  
 TGCGCTACCTGAGCCTGGATGGGAACCCCTCTAGCTGTATTGGTCCGGTGCCTCGGGGG  
 CTGGGAGGCCTTACACACCTGTCTGGCAGCCTGCAGAGGCTCCCTGAGCTGGCGCCAG  
 TGGCTCCGTGAGCTACCGGGCTGCAGGTCTGGACCTGTCGGGCAACCCCAAGCTTAAC  
 GGGCAGGAGCTGAGGTGTTTCAGGCCTGAGCTCCCTGCAAGGAGCTGGACCTTCGGGCACC  
 AACCTGGTGCCTGCCTGAGGCCTGCTCCTCACCTCCGGCACTGCAGAGCGTCAGCGT  
 GGGCCAGGATGTGCGGTGCCGGCCTGGTGCAGGGCACCTACCCCCGGAGGCCTGGCT  
 CCAGCCCCAAGGTGCCCTGCACTGCGTAGACACCCGGGAATCTGCTGCCAGGGGCCACC  
**ATCTTG****TGA**CAAATGGTGTGGCCAGGGCACATAACAGACTGCTGTCCTGGCTGCCTCAG  
 GTCCCAGGTACTTATGTTCAATGTGCCAACACCAACTGGGAGGCCGCAGGCCTATGTGGCA  
 GCGTCACCACAGGAGTTGTGGGCTAGGAGAGGCTTGGACCTGGGAGGCCACACCTAGGAGC  
 AAAGTCTCACCCCTTGCTACGTTGCTTCCCAAACCATGAGCAGAGGGACTTCGATGCCA  
 AACCAGACTCGGGTCCCCCTGCTTCCCTCCCCACTTATCCCCAAGTGCCTCCCTCAT  
 GCCTGGGCCGGCCTGACCCGCAATGGCAGAGGGTGGGTGGGACCCCTGCTGCAGGGCAGA  
 GTTCAGGTCCACTGGGCTGAGTGTCCTTGCCATGGGCCATGAGGCCATTCAGGGCGAGTT  
 TCTTTCTAACATAGCCCTTCTTGCCATGAGGCCATGAGGCCATTCATCCTTTCTAT  
 TTCCCTAGAACCTTAATGGTAGAAGGAATTGCAAAGAATCAAGTCCACCCCTCTCATGTGAC  
 AGATGGGAAACTGAGGCCCTGAGAAGGAAAAGGCTAATCTAAGTCCCTGCCGGCAGTGGC  
 ATGACTGGAGCACAGCCTCTGCCCTCCCAGCCGGACCCAAATGCACTTCTGTCTCCTCTA  
 ATAAGCCCCACCCCTCCCCGCCTGGCTCCCTGCTGCCCTGCTGTTCCCCATTAGCACA  
 GGAGTAGCAGCAGCAGGACAGGCAAGAGCCTCACAGTGGACTCTGGGCCTGACAGCT  
 GTGCCGCATGGCTAAAGTCACTGCCCTCGGAGCCTCTGGAAGCTAGGGCACATTGGTT  
 CCAGCCTAGCCAGTTCTACCCCTGGGTGGGCTCCCGAGCATCCAGACTGGAAACCTACC  
 CATTTCCTGAGCATCCTCTAGATGCTGCCCAAGGAGTGTGCAAGTCTGGAGCCTCA  
 TCTGGCTGGATCTCAAGGGCCTCTGGATTCACTGCCCCACTGCCCTGAGCACGACAGC  
 CCTTCTTACCCCTCCAGGAATGCCGTGAAAGGAGACAAGGTCTGCCGACCCATGTCTATGC  
 TCTACCCCCAGGGCAGCATCTCAGCTCCGAACCCCTGGCTGTTCTTAGTCTTCAATTAA  
 TAAAAGTTGTTGCCCTTTAACGGAGTGTCACTTCAACCGGCCTCCCTACCCCTGCTGGC  
 CGGGGATGGAGACATGTCAATTGAAAAGCAGAAAAAGGTTGCATTGTTCACTTTGTAAT  
 ATTGTCTGGCCTGTGTTGGGGTGGGGAGCTGGCAGTCAGTGGCCACATGGCCTAGC  
 AGGGGCTGGCCCCACAGAGACCCACAGGGCAGTGTCTGCTCCCCACACTGCCCTAGC  
 CCATCATCTAACCGGTCTTGATTAAACACTATAAAAGTTAAAAAAAAAAAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 232**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652
><subunit 1 of 1, 353 aa, 1 stop
><MW: 37847, pI: 6.80, NX(S/T): 2
MPWPLLLLLAVSGAQTTTRPCFPGCQCEVETFGLFDSFSLDRVDCSGLGPHIMPVPIPLDTAH
LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLLTSISPTAFSRLRYLESLDLSHNGLTALP
AESFTSSPLSDVNLSHNQLREVSVAFTTHSQGRALHVDLSHNLIHRLVPHPTRAGLPAPTI
QSLNLAWNRLHAVPNLRDPLRYYLSLDGNPLAVIGPGAFAGLGGLTHLSSLASLQRQLPELAPS
GFRELPGLQVLDSLGNPKLNWAGAEVFSGLSSLQELDLSGTNLVPLPEALLLHLPALQSVSV
GQDVRCRRLVREGTYPRRPGSPPKVLHCVDTRESAARGPTIL
```

**Signal peptide:**

amino acids 1-16

**Transmembrane domains:**

amino acids 215-232, 287-304

## **FIGURE 233**

GATGGCGCAGCCACAGCTCTGTGAGATTGATTCTCCCCAGTTCCCCTGTGGGTCTGAGG  
 GGACCAAGGGTGAGCTACGTTGGCTTCTGGAAGGGGAGGGCTAT**ATG**CGTCAATTCCCCA  
 AAACAAGTTTGACATTCCCCTGAAATGTCATTCTATCTATTCACTGCAAGTGCCTGCT  
 GTTCCAGGCCTTACCTGCTGGGACTAACGGCGGAGGCCAGGATGGGGACAGAATAAAGGAGC  
 CACGACCTGTGCCACCAACTCGCACTCAGACTCTGAACCTCAGACCTGAAATCTCTTCA  
 GGGAGGCTTGGCAGTTTCTTACTCCTGTGGTCTCCAGATTTCAGGCCTAAGATGAAAGCC  
 TCTAGTCTGCCTTCAGCCTCTCTGCTGCGTTTATCCTATGGACTCCTCCACTGG  
 ACTGAAGACACTCAATTGGGAAGCTGTGATGCCACAAACCTCAGGAAATACGAAATG  
 GATTTCTGAGATA CGGGGAGTGTGCAAGCCAAGATGAAACATGACATCAGAATCTTA  
 AGGAGGACTGAGTCTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCGGCCATT  
 GCTAAGACTCTATCTGGACAGGGTATTTAAAAACTACCAGACCCCTGACCATTACTCTCC  
 GGAAGATCAGCAGCCTGCCAATTCTTCTTACCATCAAGAAGGACCTCCGGCTCTCAT  
 GCCCACATGACATGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCA  
 CTTTGAAGCTGGAACCTCAGGCAGCAGTGTGAAGGCTTGGGGAACTAGACATTCTTC  
 TGCAATGGATGGAGGAGACAGAA**TAG**GAGGAAAGTGATGCTGCTGCTAAGAATATTGAGGT  
 CAAGAGCTCCAGTCTCAATA CCTGCAGAGGAGGCATGACCCAAACCACCATCTTTACT  
 GTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTGCTTACTTGCTTCCTGCATGAT  
 TGTCTTATGCATCCCCAATCTAATTGAGACCATA TTGTATAAGATTTGTAATATCTT  
 TCTGCTATTGGATATATTATTAGTTAATATATTATTATTATTGCTATTAAATGTATTT  
 ATTTTTTACTTGGACATGAAACTTAAAAAAATTCAAGATTATTTATAACCTGACTAG  
 AGCAGGTGATGTATTTTATACAGTAAAAAAAAACCTTGTAAATTCTAGAAGAGTGGCT  
 AGGGGGTTATTCAATTGTATTCAACTAAGGACATATTACTCATGCTGATGCTCTGTGAGA  
 TATTTGAAATTGAACCAATGACTACTTAGGATGGGTGTGGAATAAGTTGATGTGGAATT  
 GCACATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTAT  
 CTTCCAGCCAGGAATCCTACACGGCCAGCATGTATTCTACAAATAAGTTTCTTGCATA  
 CCAAAAAAAAAAAAAAAA

## **FIGURE 234**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500
><subunit 1 of 1, 261 aa, 1 stop
><MW: 29667, pI: 8.76, NX(S/T): 0
MRQFPKTSFDISPEMSFSIYSLQPAVPGGLTCWALTAEPGWGQNKGATTCATNSHSDSELRP
EIFSSREAWQFFLLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNL
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTK PANRCCLLRHLLRLYLDdrvFKNYQTP
DHYTLRKISSLANSFLTICKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALG
ELDILLQWMEETE
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-42

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 192-195, 225-228

**N-myristoylation sites.**

amino acids 42-47, 46-51, 136-141

**FIGURE 235**

CCGTTATCGTCTTGCCTACTGCTGAATGTCCGTCCGGAGGAGGAGAGGCTTTGCCG  
CTGACCCAGAGATGGCCCCGAGCGAGCAAATTCTACTGTCCGGCTGCCGGCTACCGTGGC  
CGAGCTAGCAACCTTCCCCTGGATCTCACAAAAACTCGACTCCAATGCAAGGAGAACGAG  
CTCTTGCTCGGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCACACA  
GCCCTAGGGATCATTGAAGAGGAAGGCTTCTAAAGCTTGGCAAGGAGTGACACCCGCCAT  
TTACAGACACGTAGTGTATTCTGGAGGTGAATGGTCACATATGAACATCTCCGAGAGGTTG  
TGTGGCAAAAGTGAAGATGAGCATTATCCCCTTGGAAATCAGTCATTGGAGGGATGATG  
GCTGGTGTATTGCCAGTTTAGCCAATCCAACGTACCTAGTGAAGGTTCAGATGCAAAT  
GGAAGGAAAAAGGAAACTGGAAGGAAAACCATTGCGATTCGTGGTACATCATGCATTG  
CAAAATCTTAGCTGAAGGAGGAATACGAGGGCTTGGCAGGCTGGTACCCAATATAACAA  
AGAGCAGCACTGGTGAATATGGGAGATTAAACCACTTATGATAACAGTGAAACACTACTGGT  
ATTGAATAACACCACTTGAGGACAATATCATGACTCACGGTTATCAAGTTATGTTCTGGAC  
TGGTAGCTTCTATTCTGGAACACCCAGCCATGTCAAAAGCAGAATAATGAATCAACCA  
CGAGATAAACAGGAAGGGACTTTGTATAAATCATCGACTGACTGCTTGATTCAAGCTGT  
TCAAGGTGAAGGATTCATGAGTCATATAAAGGCTTTACCATCTGGCTGAGAATGACCC  
CTTGGTCAATGGTGTCTGGCTTACTTATGAAAAAATCAGAGAGATGAGTGGAGTCAGTCCA  
TTTTAA

**FIGURE 236**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568  
><subunit 1 of 1, 323 aa, 1 stop  
><MW: 36064, pI: 9.33, NX(S/T): 1  
MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMQGEAALARLGDGA  
RESAPYRGMVRTALGIIEEGFLKLWQGVTPAIYRHVVYSGGRMVTYEHLREVVFGKSEDEH  
YPLWKSVIGGMMAGVIGQFLANPTDLVKVQMOMEGKRKLEGKPLRFRGVHHAFAKILAEGGI  
RGLWAGWVPNIQRAALVNMGDLTTYDTVKHYLVNTPLEDNIMTHGLSSLCGLVASILGTP  
ADVIKSrimNQPRDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFLPSWLRTMPWSMVFWLT  
YEKIREMSGVSPF

**Transmembrane domains:**

amino acids 25-38, 130-147, 233-248

## **FIGURE 237**

CGGACCGCGGGCGCGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCCTCCTGCAGCGC  
 GCCTGAAGTCGGCGTGGCGTTGAGGAAGCTGGATACAGCATTAAATGAAAAATTATGC  
 TTAAGAAGTAAAAATGGCAGGCTCCTAGATAATTCGTTGGCCAGAATGTGAATGTATTG  
 ACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGCGCAGGTATATTGTTTACAGGC  
 TGGTGGATAATGATTGATGCAGCTGTGGTATCCTAACAGCCAGAACAGTTGAACCATGCC  
 TCACACATGTGGTGTATTTCCACATTGGCTTCTCATGATAAATGCTGTATCCAATGCTC  
 AGGTGAGAGGTGATAGCTATGAAAGCGGCTGTTAGGAAGAACAGGTGCTCGAGTTGGCTT  
 TTCATTGGTTCATGTTGATGTTGGTCACTTATTGCTTCCATGTGGATTCTTTGGTGC  
 ATATGTTACCCAAAATACTGATGTTATCCGGGACTAGCTGTGTTTCAAAATGCACCTA  
 TATTTTAGCACTCTGATCTACAAATTGGAAGAACCGAAGAGCTATGGACCTGAGATCAC  
 TTCTTAAGTCACATTTCTTTGTTATTCTGTTAGATAGGTTTATCTCAGT  
 ACACATTGCCAAATGGAGTAGATTGTACATTAAATGTTGTTCTTACATTTATGTC  
 TGAGTTGAAATAGTTATGAAATTCTTATTTCATGCATAGACTGTTAATATGTA  
 TATAATACAAGACTATATGAAATTGGATAATGAGTATCAGTTTATTCCCTGAGATTAGAA  
 CTTGATCTACTCCCTGAGCCAGGGTACATCATCTGTCATTAGAAGTAACCACTCTGT  
 CTCTCTGGCTGGCACGGTGGCTCATGCCTGTAATCCCAGCACTTGGGAGGCCGAGGCC  
 CCGATTGCTTGAGGTCAAGTGTGTTGAGACCAGCCTGCCAACATGGCGAAACCCATCTACT  
 AAAAATACAAAAATTAGCCAGGCATGGTGGTGGTGCCTGTAATCCCAGCTACCTGGGAGGC  
 TGAGGCAGGAGAATCGCTGAACCCGGGGGGCAGAGGTTGCAGTGAGCTGAGTTGCCAC  
 TGCACCTAGCCTGGGGAGAAAGTGAACACTCCCTCTCAAAAAAAAGACCACTCTCAGTATC  
 TCTGATTCTGAAGATGTACAAAAAATAGCTTCATATCTGGAATGAGCACTGAGCCA  
 TAAAAGGTTTCAGCAAGTTGTAACCTATTTGGCCTAAAATGAGGTTTTGGTAAAGA  
 AAAAATATTGTTCTTATGTATTGAAGAAGTGTACTTTATATAATGATTTTAAATGCC  
 AAAGGACTAGTTGAAAGCTTCTTAAAAAGAATTCCCTCTAATATGACTTATGTGAGAA

## **FIGURE 238**

MAGFLDNFRWPECECIDWSERRNAVASVAGILFFTGWWIMIDAAVVYPKPEQLNHAFHTCG  
VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIGFMLMFGSLIASMWILFGAYVTQ  
NTDVYPGLAVFFQNALIFFSTLIYKFGRTEELWT

**Important features:**

**Signal peptide:**

amino acids 1-44

**Transmembrane domains:**

amino acids 23-42 (type II), 60-80, 97-117, 128-148

## **FIGURE 239**

GTTGATGGCAAACCTCCTCAAAGGAGGGCAGAGCCTGCGCAGGCAGGAGCAGCTGGCCA  
 CTGGCGGCCCGCAACACTCCGTCTCACCTCTGGCCCAGTCATCTAGAGGAGGGCGTCT  
 GTGAGGCCACTACCCCTCCAGCAACTGGGAGGTGGACTGTCAGAAGCTGGCCCAGGGTGGT  
 GGTCAAGCTGGGTCAAGGACCTACGGCACCTGCTGGACCACCTGCCTCTCCATCGAAGCAG  
 GGAAGTGGGAGCCTCGAGCCCTGGGTGGAAGCTGACCCCAAGCCACCCACCTGGACAG  
**GATG**AAGAGTGTCAAGGTGTGCTTCGCCTCCTGGCCCATCTTGCCATAGTCACGACATGGA  
 TGTATTGCAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCA  
 GCCTCGCCCACCAAGGAGATCCAGGTTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCC  
 AGCCAACTAACTTGCGTTAAATCTGCAGTGGGCCAACGTCGTGGCCCTACTATGT  
 GCTTGAAGACCGCATGATCATGAGTCCTGTGAAAAACAATGTGGCAGAGGCCTAACATC  
 GCCCTGGTGAATGGAACCACGGAGCTGTGCTGGACAGAAGGCATTGACATGTACTCTGG  
 AGATGTTATGCACCTAGTGAAATTCTTAAAGAAATTCCGGGGGTGCACTGGTGCTGGTGG  
 CCTCCTACGACGATCCAGGGACCAAAATGAACGATGAAAGCAGGAAACTCTCTGACTTG  
 GGGAGTCCCTACGCAAACAACTGGCTTCCGGACAGCTGGTCTTCATAGGAGCCAAGA  
 CCTCAGGGTAAAGCCCTTGAGCAGTTCTAAAGAACAGCCAGACACAAACAAATACG  
 AGGGATGGCCAGAGCTGCTGGAGATGGAGGGCTGCATGCCCGAAGCCATT**TAG**GGTGGC  
 TGTGGCTTCCCTCAGCCAGGGCCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCCG  
 GCAGGGCTGAGGAGGAGCAGGGGTGCTGCGTGGAAAGGTGCTGCAGGTCTTGCACGC  
 TGTGTCGCGCCTCTCCTCGAAACAGAACCCCTCCCACAGCACATCCTACCCGGAAGACC  
 AGCCTCAGAGGGCTTCTGGAACCAGCTGTCTGTGGAGAGAATGGGTGCTTCGTCAAGG  
 ACTGCTGACGGCTGGCCTGAGGAAGGACAAACTGCCAGACTTGAGCCCAATTAAATTAA  
 TTTTGCTGGTTTGAAAAAAAAAAAAAA

1 0 0 1 5 6 1 0 9 1 2 1 0 7

## **FIGURE 240**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814
<subunit 1 of 1, 224 aa, 1 stop
<MW: 24963, pI: 9.64, NX(S/T): 1
MRVSGVLRLALIFAIVTWMFIRSYMSFSMKTIRLPRWLAASPTKEIQVKKYKCGLIKPCP
ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNGRGLNIALVNNGTTGAVLGQKAFDMYSG
DVMHLVKFLKEIPGGALVLVASYDDPGTKMNDESRKLFSDLGSSYAKQLGFRDSWVFIGAKD
LRGKSPFEQFLKNSPDTNKYEGWPELLEMEGCMPPKPF
```

**Important features:**

**Signal peptide:**

amino acids 1-15

**ATP/GTP-binding site motif A (P-loop).**

amino acids 184-191

**N-glycosylation site.**

amino acids 107-110

## **FIGURE 241**

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGAGATTGTCCTGGGGAT  
 CCAGAAACCCATGATAACCCTACTGAACACCGAACATCCCCTGGAAGGCCACAGAGACAGAGACA  
 GCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCTC  
 TCACTCCTCCCTCCCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTCCCAGTCCC  
 CTGCACCCCTTCCGGACACTATGTTGTTCTCCGCCCTGCTGGAGGTGATTGGATCC  
 TGGCTGCAGATGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAGGACCATTGGCCA  
 GCCTCTTACCCCTGAGTGAAACAATGCCAGTCGCCATCGATATTCAAGACAGACAGTGT  
 GACATTGACCCCTGATTGCTGCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGC  
 CTTTGGACCTGCACAACAATGCCACACAGTCAACTCTCTGCCCTCACCTGTATCTG  
 GGTGGACTTCCCCGAAAATATGTAGCTGCCAGCTCCACCTGCACTGGGTAGAAAGGATC  
 CCCAGGGGGTCAGAACACCAGATCAACAGTGAAGCCACATTGCAAGAGCTCCACATTGTAC  
 ATTATGACTCTGATTCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGGCTGGCT  
 GTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAG  
 TCACTGCATGAAGTCAGGCATAAAGATCAGAAGACCTCAGTGCCTCCCTCAACCTAACAGAG  
 AGCTGCTCCCCAACAGCTGGGCAGTACTCCGCTACAATGGCTCGCTACAACACTCCCCCT  
 TGCTACCAGAGTGTGCTGGACAGTTTATAGAAGGTCCCAGATTCAATGGAACAGCT  
 GGAAAAGCTTCAGGGACATTGCTCCACAGAACAGAGGAGCCCTTAAGCTCTGGTACAGA  
 ACTACCGAGCCCTCAGCCTCTCAATCAGCGCATGGCTTGCTTCAAGCAGGA  
 TCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGAGGAATCTGGTTGGCTGTCTG  
 CCTTCTCCTGGCTTTATTCATTGCTAGAAAGATTGGAAGAACAGAGGCTGGAAAACCGAA  
 AGAGTGTGGCTTCACCTCAGCACAAGCCACGACTGAGGCATAAATTCTCTCAGATACCA  
 TGGATGTGGATGACTTCCCTCATGCCTATCAGGAAGCCTCTAAATGGGTGAGGATCTG  
 GCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCCTCCCTGGACATCTTAGAGAG  
 GAATGGACCCAGGCTGTCATTCCAGGAAGAACTGCAGAGCCTCAGCCTCTCCAAACATGTA  
 GGAGGAAATGAGGAATCGCTGTGTTAATGCAGAGANCAAACCTGTTAGTTGCAGGG  
 GAAGTTGGATATAACCCAAAGCCTCTACCCCTCACTTTATGCCCTTCCCTAGATA  
 TACTGCGGGATCTCTCCTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTGATCAATA  
 TATTGGAAATTAAAGTTCTGACTTT

**FIGURE 242**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812
><subunit 1 of 1, 337 aa, 1 stop
><MW: 37668, pI: 6.27, NX(S/T): 1
MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLP
ALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQ
INSEATFAELHIVHYDSDSYDSLSEAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRH
KDQKTSVPPFNLRELLPKQLGQYFRYNGSLTPPCYQSVLWTVFYRRSQISMEQLEKLQGTL
FSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYF
IARKIRKKRLENRKSVVFTSAQATTEA
```

**Important features of the protein:****Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 291-310

**N-glycosylation site.**

amino acids 213-216

**Eukaryotic-type carbonic anhydrases proteins**

amino acids 197-245, 104-140, 22-69

## **FIGURE 243**

## **FIGURE 244**

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSSLIPLTQM  
LTLPDLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPFVTQLGAQGTILSSEE  
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLPTPSG  
TDDDFAVTPAGIQRSTHAIIEATTESANGIQ

**Signal peptide:**

amino acids 1-16

**FIGURE 245**

GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCG  
GAGCCAGACGCTGACCACGTTCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCCTGCCCG  
GCAGCCGGGAGCC**ATG**CGACCCCAGGGCCCCGCCCTCCCGCAGCGGCTCCGCGGCCTCC  
TGCTGCTCCTGCTGCTGCAGCTGCCGCCGTGAGCGCCTCTGAGATCCCCAAGGGGAAG  
CAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGG  
GCCAGCAGGAGTGCCTGGTCGAGACGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTG  
GGATCCCAGGTGGGATGGATTCAAAGGAGAAAAGGGGAATGTCAGGGAAAGCTTGAG  
GAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTCATTGAATTATGGCATAGATCT  
TGGGAAAATTGCGGAGTGTACATTACAAAGATGCGTCAAATAGTGCCTAAAGAGTTTGT  
TCAGTGGCTCACTCGGCTAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTCACATTC  
AATGGAGCTGAATGTTCAAGGACCTCTCCATTGAAGCTATAATTATTGGACCAAGGAAG  
CCCTGAAATGAATTCAACAATTAATATTCACTGCACCTCTGTGGAAGGACTTGTGAAG  
GAATTGGTGTGGATTAGTGGATGTTGCTATCTGGTTGGCACTTGTTCAGATTACCCAAA  
GGAGATGCTTCACTGGATGGAATTCAAGTTCTCGCATCATTATTGAAGAACTACCAAA**TA**  
**A**ATGCTTTAATTTCTACCTCTTTTATTATGCCTTGAATGGTCACTTAAAT  
GACATTTAAATAAGTTATGTATACTGAATGAAAAGCAAAGCTAAATATGTTACAGA  
CCAAAGTGTGATTCACACTGTTTAAATCTAGCATTATTCACTTGTCAATCAAAAGT  
GGTTCAATATTTTTAGTTGGTTAGAATACTTCTCATAGTCACATTCTCAACCTA  
TAATTGGAATATTGTTGTGGCTTTGTTCTTAGTATAGCATTAAAAAAATA  
AAAAAGCTACCAATCTTGTACAATTGTAAATGTTAAGAATTAAAAATCTGTTAAAT  
AAAAATTATTCCAACA

## **FIGURE 246**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393
><subunit 1 of 1, 243 aa, 1 stop
><MW: 26266, pI: 8.43, NX(S/T): 1
MRPQGPAA SPQR LRG LLLL LQL PAPSSA SEIPKG KQKA QL RQ REVVDLY NGMCL QGPAGV
PGRDGSPGANV IPGT PGIP GRDG FKGE KGE CLRESFEE SWTP NYKQ CSWSSL NYGIDL GKIA
ECTFTKMR SNSAL RVLF SGSL RLKCRN ACCQRW YFTFNG AEC SGPLPI EAI IYLDQGSPE MN
STINI HRTSS VEGL CEGIGA GLVDV AIWVGTCSDYPKGDASTGW NSVSRIII EELPK
```

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217